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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:14:12 ; Search time 6073.61 Seconds
(without alignments)
4455.779 Million cell updates/sec

Title: US-08-656-055-18
Perfect score: 5288
Sequence: 1 GAATTCGCCGCGACCGCAAG.....TATGAAGAAAGCCCGAAT 5288

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 255875100 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_ba2:*
3: gb_cm:*
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5: gb_ph:*
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83: em_hc90:*
84: gb_hc24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	5288	100.0	5288	81	AR055796
2	4681.6	88.5	6568	53	HSU43148
3	4344	82.1	4344	53	HSU59464
4	3801.2	71.9	5187	81	AR055788
5	3801.2	71.9	5187	81	AR055791
6	3484.2	65.9	4305	11	MMU46155
7	2790.4	52.8	4502	4	GGU40074
8	1965	37.2	3732	4	DRE007742
9	1532.8	29.0	2066	11	AF079162
10	1362.2	25.8	3672	4	DRP47CH
11	1176.4	22.2	3612	10	AF091501
12	1171.6	22.2	3453	10	AF119569
13	1170	22.1	3612	10	AF087651
14	1164.2	22.0	3549	11	AB010833
15	565.6	10.7	160716	67	AC053475
16	565	10.7	160716	67	AC053475
17	564	10.7	194471	73	AL161729
18	559.6	10.6	145236	75	AL1392185
19	555.6	10.5	176668	65	AC027096
20	543.8	10.3	772	4	AB000848
21	433.8	8.2	2032	13	AX002313

22	411.8	7.8	3900	81	AR063104	Sequence
23	411.8	7.8	3536	32	DMP2CR	X17558 D. melanoga
24	405	7.7	4434	81	AR055789	Sequence
25	384.6	7.3	4179	31	AF117898	Sequence
26	339.2	6.4	766	4	AB000846	Junonia c
27	248.8	4.7	5665	32	DR0002	M28999 D. melanoga
28	245.6	4.6	166787	54	AC007085	Protophila
29	245.6	4.6	168701	54	AC007303	Protophila
30	245.6	4.6	172838	60	AC020451	Protophila
31	245.6	4.6	253273	30	CEZK675	Protophila
32	175.4	3.3	22703	32	AC024746	Caenorhabd
33	159.2	3.0	59320	30	AC006706	Caenorhabd
34	159.2	3.0	180664	54	CELF21H12	Caenorhabd
35	139.8	2.6	21805	31	AL136380	Homo sapi
36	135.4	2.6	162356	72	MTV017	Myobacte
37	92.6	1.8	67200	2	MTV017	Myobacte
38	86.2	1.6	40790	2	MTV017	Myobacte
39	83.8	1.6	85388	63	AC024907_3	Myobacte
40	83.8	1.6	85388	63	AC024907_3	Myobacte
41	83.6	1.6	3941	11	RNLAR2	Continuation (4 of
42	82.4	1.6	69350	2	MTV004	X83546 R. norvegicu
43	82.4	1.6	2479	11	RNLAR2	Continuation (4 of
44	82.4	1.6	47852	2	MTV023	U87960 Rattus norv
45	81	1.5	180144	63	AC023429	AL022022 Mycobacte

ALIGNMENTS

RESULT 1
 LOCUS AR055796 5288 bp DNA
 DEFINITION Sequence 18 from patent US 5837538.
 ACCESSION AR055796
 VERSION AR055796.1 GI:5981373
 KEYWORDS
 SOURCE Unknown.

REFERENCE 1 (bases 1 to 5288)
 AUTHORS Scott, M.P., Goodrich, L.V., and Johnson, R.L.
 TITLE Patched genes and their use
 JOURNAL Patent: US 5837538-A 18 17-NOV-1998;
 FEATURES
 Location/Qualifiers
 source 1..5288

BASE COUNT 1182 a 1530 c 1417 g 1159 t
 ORIGIN

Query Match 100.0%; Score 5288; DB 81; Length 5288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGAGCGCAAGAGAGTGGCGGAGCGCGCAAGAGAGAGGCTCGCGGCGC 60
 Db 1 GAATTCGGGGAGCGCAAGAGAGTGGCGGAGCGCGCAAGAGAGAGGCTCGCGGCGC 60
 QY 61 GCGGCTCTGCTCTTCCGCAACTGATGTGGGCAAGCGCGCGCGAGACCTCGGGA 120
 Db 61 GCGGCTCTGCTCTTCCGCAACTGATGTGGGCAAGCGCGCGCGAGACCTCGGGA 120
 QY 121 CCCCCGCAATGTGGCAATGGAAGGCGGAGGCTGACTCCCGCGAGCGCGCGCGCGC 180
 Db 121 CCCCCGCAATGTGGCAATGGAAGGCGGAGGCTGACTCCCGCGAGCGCGCGCGCGC 180
 QY 181 GCAGCGGAGACGCGCGCGCGGTGTGAGCAGCAGCAGGCGGTGTGTCAACCGAGGC 240
 Db 181 GCAGCGGAGACGCGCGCGCGGTGTGAGCAGCAGCAGGCGGTGTGTCAACCGAGGC 240
 QY 241 CGAGCGGAGACGCGGTGTGAGCAGCAGGCTGTGCAAGCGGAGCGCGCGCGGC 300
 Db 241 CGAGCGGAGACGCGGTGTGAGCAGCAGGCTGTGCAAGCGGAGCGCGCGCGGC 300

QY 301 GAGCCGAGCAGCGCGGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 360
 Db 301 GAGCCGAGCAGCGCGGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 360
 QY 361 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 420
 Db 361 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 420
 QY 421 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 480
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 QY 541 CCAGCTACTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 600
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 QY 601 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 660
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 QY 721 CGGTGGGATTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
 Db 721 CGGTGGGATTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
 QY 781 GAGGACGAGTACGTGCGTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
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 QY 841 TTAATCTCAATCATGATACAGACCCCTAAAGAAAGAGTGTAAATCTCGACACAG 900
 Db 841 TTAATCTCAATCATGATACAGACCCCTAAAGAAAGAGTGTAAATCTCGACACAG 900
 QY 901 AAGCGCTCTCAACACCTGAGCTCGGACCTCAAGCGCGCGCGCGCGCGCGCGCGC 960
 Db 901 AAGCGCTCTCAACACCTGAGCTCGGACCTCAAGCGCGCGCGCGCGCGCGCGCGC 960
 QY 961 ACAACAGCAGTGAATTTGAACATTTGTTTCAATTCAGAGAGAGTGTATACAGAA 1020
 Db 961 ACAACAGCAGTGAATTTGAACATTTGTTTCAATTCAGAGAGAGTGTATACAGAA 1020
 QY 1021 CAGGTTACATGATCAGATATAGATATATATATATATATATATATATATATATAT 1080
 Db 1021 CAGGTTACATGATCAGATATAGATATATATATATATATATATATATATATATAT 1080
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 QY 1201 ATCAAGTGAACAGCTGGGAGAAATGCTGAATAGAGTGTGATGATGATGATGATG 1260
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 QY 1261 ACCGCGCGCTGCTCATTCGCGCGCGGATCGAGACTGCGCGCGCGCGCGCGCGCGC 1320
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 QY 1321 CAACCAAACTCTTGAATAGGCGCTTGTGATGATGATGATGATGATGATGATGATG 1380
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QY 1381 AGTATATGCACTGGCAGAGAGACTTGAATGTGGGTGGCAGACATGACAAAGCACTGCAA 1440
DB 1381 AGTATATGCACTGGCAGAGAGAGACTTGAATGTGGGTGGCAGACATGACAAAGCACTGCAA 1440
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DB 1501 ACAGAGCACTTCAAGGGGTAGAGATGTCTCACACATCACTGGAACAGAGCAAAAGCG 1560
QY 1561 CACCCATCCCTGGAGAGCGCTGCAGAGACATATGTGGAGGTGTTTCATCAGAGTGCAC 1620
DB 1561 CACCCATCCCTGGAGAGCGCTGCAGAGACATATGTGGAGGTGTTTCATCAGAGTGCAC 1620
QY 1621 AGAATCTCACTCAAAAGGTTGTTCTTCAACACACAGACCTGGAGCAATCCGAAAT 1680
DB 1621 AGAATCTCACTCAAAAGGTTGTTCTTCAACACACAGACCTGGAGCAATCCGAAAT 1680
QY 1681 CCTTCTCTGACAGTCAATGTATCCGCGTGGCCAGCGGCTACTTACTATGCTGCGCTATG 1740
DB 1681 CCTTCTCTGACAGTCAATGTATCCGCGTGGCCAGCGGCTACTTACTATGCTGCGCTATG 1740
QY 1741 CCGTCTAACCAATGCTCGCTGGAGAGTCTTCAAGTCCAGAGTCCGTGGGCGTGGCTG 1800
DB 1741 CCGTCTAACCAATGCTCGCTGGAGAGTCTTCAAGTCCAGAGTCCGTGGGCGTGGCTG 1800
QY 1801 GCGTCCCTGCTGTGACAGTGTCACTGAGTGGCTGCAGAGACTGGGCTGGCTGATGATCGAA 1860
DB 1801 GCGTCCCTGCTGTGACAGTGTCACTGAGTGGCTGCAGAGACTGGGCTGGCTGATGATCGAA 1860
QY 1861 TTTCTCTTAAAGCTGCAACAACATCAGTTTGGCATTCTTCTGCTTGGTGGTGGT 1920
DB 1861 TTTCTCTTAAAGCTGCAACAACATCAGTTTGGCATTCTTCTGCTTGGTGGTGGT 1920
QY 1921 ATGATGTTTTCTTCTTCTGCGCCAGCGCTTCAATGAAACAGAGCAATATAAGATCCCTT 1980
DB 1921 ATGATGTTTTCTTCTTCTGCGCCAGCGCTTCAATGAAACAGAGCAATATAAGATCCCTT 1980
QY 1981 TTGAGGACAGAGCGGGGAGTGGCTGAAAGCGACAGAGAGCGAGGCTGCGCTCACTGCA 2040
DB 1981 TTGAGGACAGAGCGGGGAGTGGCTGAAAGCGACAGAGAGCGAGGCTGCGCTCACTGCA 2040
QY 2041 TCAGCAATGTACAGACCTTCTTCAATGAGCGCGGTTAATCCCAATTCGCCCTGCGGGGT 2100
DB 2041 TCAGCAATGTACAGACCTTCTTCAATGAGCGCGGTTAATCCCAATTCGCCCTGCGGGGT 2100
QY 2101 TCTCCCTCCAGGCGAGGCTGTAGTGTGTTCAATTTTGGCATGGTCTGCTCATTTTTC 2160
DB 2101 TCTCCCTCCAGGCGAGGCTGTAGTGTGTTCAATTTTGGCATGGTCTGCTCATTTTTC 2160
QY 2161 CTGCAATTTCTAGCATGATGATTTATGAGCGAGAGAGAGATGATATTTTCTGCT 2220
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QY 2221 GTTTTACAAAGCCCTGCGTACAGAGATGATTTCAAGTTGAACTCAGGCTTACACGACA 2280
DB 2221 GTTTTACAAAGCCCTGCGTACAGAGATGATTTCAAGTTGAACTCAGGCTTACACGACA 2280
QY 2281 CACAGCAATACCGGCTGACAGAGCTTCAAGTTGAACTCAGGCTTACACGACA 2340
DB 2281 CACAGCAATACCGGCTGACAGAGCTTCAAGTTGAACTCAGGCTTACACGACA 2340
QY 2341 AAAGCGATTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
DB 2341 AAAGCGATTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
QY 2401 ACCTGTACTACACACCGCTGAGCGGCTCCGAGATCTCTGTGAGGCGCGTCAACGCTGA 2460
DB 2401 ACCTGTACTACACACCGCTGAGCGGCTCCGAGATCTCTGTGAGGCGCGTCAACGCTGA 2460
QY 2461 CACAGGACACCTTACGCTGCCAGAGCCAGAGACACCAAGCTCCACAAGGACCTGCTCT 2520

DB 2461 CACAGGACACCTTACGCTGCCAGAGCCAGAGAGACACACACTCCACAAGGACCTGCTCT 2520
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DB 2521 CCAGTTCTTCGACCTCAGAGCTCAGTGGCTGAGGCCCTCTGAGCAAGTGGACACTCT 2580
QY 2581 CATCTTTTCTGAGAGACACTATGCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 2640
DB 2581 CATCTTTTCTGAGAGACACTATGCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 2640
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DB 2641 TGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 2700
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DB 2701 ACAGGCTGACCTTACGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
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QY 2941 AGGACCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
DB 2941 AGGACCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
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DB 3001 ACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
QY 3061 GCGATTAAGCCATGACATGACAGCTGATGATGATGATGATGATGATGATGATGATGATG 3120
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DB 3241 CCGATGCTGCTTCCAGGCGCAACATCCGCGCACACCGACAGATGAGTCCACGACAAAG 3300
QY 3301 AGTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3360
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QY 3361 AAGTAAAGACATCTGACAGCACTATGAGAGCTGGGCTGTCTGATTTACCCCAAGGCT 3420
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QY 3421 ACCCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3480
DB 3421 ACCCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3480
QY 3481 GCGTGTGTTGGCTCACAATTCCTGTGCGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3540
DB 3481 GCGTGTGTTGGCTCACAATTCCTGTGCGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3540
QY 3541 CCGGGATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600

Db	3541	CCGGGATCATTGGATGGTCCCTGGCGGTGATGAGGGGCGAGCTGTTCGGCATGATGGGCC	3601
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Db	3601	TCATGGGAATCAAGCTCAGTGGCGGTGGCTGGTCACTCGATCGCTTCTGTGGCATAG	3660
Qy	3661	GAGTGGAGTTTACCGTTTACAGGTTTGGCTTTTCTGAGGGGCATGGGGACAAAGAAC	3720
Db	3661	GAGTGGAGTTTACCGTTTACAGGTTTGGCTTTTCTGAGGGGCATGGGGACAAAGAAC	3720
Qy	3721	GGAGGGCTGTGCTTGGCCTGGAGACATGTTTGACCCGTCTCGAATGGGGCCCTGTCCA	3780
Db	3721	GGAGGGCTGTGCTTGGCCTGGAGACATGTTTGACCCGTCTCGAATGGGGCCCTGTCCA	3780
Qy	3781	CTCTGTGGGAGTGTGTGATGCTGTGGCGGATCTAGTTCGACTTATTTGTACGATTTCT	3840
Db	3781	CTCTGTGGGAGTGTGTGATGCTGTGGCGGATCTAGTTCGACTTATTTGTACGATTTCT	3840
Qy	3841	TTTGCTGTGGGGAGTCTGACATCTGTGGGGTTTCTCAATGGGGCTGTGTGCTCCG	3900
Db	3841	TTTGCTGTGGGGAGTCTGACATCTGTGGGGTTTCTCAATGGGGCTGTGTGCTCCG	3900
Qy	3901	TGCTTTTGTCTTCTTTTGGACATATCTGAGGGTGTCTCCAGCCAAAGGCTTGAACGCC	3960
Db	3901	TGCTTTTGTCTTCTTTTGGACATATCTGAGGGTGTCTCCAGCCAAAGGCTTGAACGCC	3960
Qy	3961	TGCCCCACACCTTCCCTGAGACCACCCCCAGCGTGTGCTGGCATGCGCCGGCC	4020
Db	3961	TGCCCCACACCTTCCCTGAGACCACCCCCAGCGTGTGCTGGCATGCGCCGGCC	4020
Qy	4021	ACACGCACACGGGGTGTGATTCCTCGACATCGGAGTATTAATTCCACACGACATGTTCAG	4080
Db	4021	ACACGCACACGGGGTGTGATTCCTCGACATCGGAGTATTAATTCCACACGACATGTTCAG	4080
Qy	4081	GGCTGACGAGGAGCTTTCGACATACGAGGGCCACGAGAGGGCGGGGAGGCGCTGCCACC	4140
Db	4081	GGCTGACGAGGAGCTTTCGACATACGAGGGCCACGAGAGGGCGGGGAGGCGCTGCCACC	4140
Qy	4141	AGTGTATGTGTGAAGCCACAGAAACCCGCTTTCGCCCACTCGTGTGTTCATCCG	4200
Db	4141	AGTGTATGTGTGAAGCCACAGAAACCCGCTTTCGCCCACTCGTGTGTTCATCCG	4200
Qy	4201	AATTCAGGAGTATACCCACCCCTGGAACCCGAGACAGAGCCCACTGTGGACTCAGAGTCCC	4260
Db	4201	AATTCAGGAGTATACCCACCCCTGGAACCCGAGACAGAGCCCACTGTGGACTCAGAGTCCC	4260
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Db	4261	TGCTTCCGGAGGCGCAAGGCGACAGCCCCGAGGGACCCCCCAGAGAGGCTTGTGGC	4320
Qy	4321	CACCCCTCTACAGACCCGCGCAGAGACGCTTTTGAATTTCTACTGAAGGGCATTTGGCC	4380
Db	4321	CACCCCTCTACAGACCCGCGCAGAGACGCTTTTGAATTTCTACTGAAGGGCATTTGGCC	4380
Qy	4381	CTAGCAATTTGGGCGCGGTGGGGCCCTCGGGGGCCGCTTCAACACCTTCGGAAACCCAG	4440
Db	4381	CTAGCAATTTGGGCGCGGTGGGGCCCTCGGGGGCCGCTTCAACACCTTCGGAAACCCAG	4440
Qy	4441	CGTCCACTGCAATTTGGGCACTCCGTGCCGGCTACTGACAGCCCACTACACACTGTGACGG	4500
Db	4441	CGTCCACTGCAATTTGGGCACTCCGTGCCGGCTACTGACAGCCCACTACACACTGTGACGG	4500
Qy	4501	CTTGTGCTCTCGTGACTGTGCGCGTGCACCCGCGCTGTCCCTTGGGCTGTGGGGGGAAC	4560
Db	4501	CTTGTGCTCTCTCGTGACTGTGCGCGTGCACCCGCGCTGTCCCTTGGGCTGTGGGGGGAAC	4560
Qy	4561	CCCCGAGGGGAGCTTTCGACAGGCTACCTCGAGACTACACACGGCTGTGTGAGAGCCCCC	4620
Db	4561	CCCCGAGGGGAGCTTTCGACAGGCTACCTCGAGACTACACACGGCTGTGTGAGAGCCCCC	4620
Qy	4621	ACGTGCTTTTTCACGTCGCGGTGTGAGAGGAGGATTCGAAAGGTGGAAAGTATTTAGCTGC	4680
Db	4621	ACGTGCTTTTTCACGTCGCGGTGTGAGAGGAGGATTCGAAAGGTGGAAAGTATTTAGCTGC	4680

QY	4681	AGGACGTGGAAATGCGACGAGAGAGGCCGCCGGGGAAGAGCGTCCAACTGACGGTGATTTAAAT	4740
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QY	4741	CTGAAGCAAGAAGSCCAAGAATTTGGAAACCCCCACCCCCACCTCTTTCCAGAACTGCTT	4800
Db	4741	CTGAAGCAAGAAGSCCAAGAATTTGGAAACCCCCACCCCCACCTCTTTCCAGAACTGCTT	4800
QY	4801	GAAGAGCACTGGTGGAAATTTAGGAAAGATGCCCTGTGGCAGAGACAGCACTGATTTGTT	4860
Db	4801	GAAGAGCACTGGTGGAAATTTAGGAAAGATGCCCTGTGGCAGAGACAGCACTGATTTGTT	4860
QY	4861	ACTGTAAACCGATTTGATATTTTGTAAATATTTTCTATAAATATTTTAAAGAGATGTACACA	4920
Db	4861	ACTGTAAACCGATTTGATATTTTGTAAATATTTTCTATAAATATTTTAAAGAGATGTACACA	4920
QY	4921	TGTGTAAATATAGGAAGAAGAGATGTAAGTGTATGATCTGGGCGTCTCCACTCTGCC	4980
Db	4921	TGTGTAAATATAGGAAGAAGAGATGTAAGTGTATGATCTGGGCGTCTCCACTCTGCC	4980
QY	4981	CCAGAGTGTGGAGGCGACAGTGGGGCCCTCCGATTTGTGSCATTTGGGCTCCGGCCACA	5040
Db	4981	CCAGAGTGTGGAGGCGACAGTGGGGCCCTCCGATTTGTGSCATTTGGGCTCCGGCCACA	5040
QY	5041	ACCAAGCTTCATATAGTCTTAAATTTTCACACATATGTTGCTGCGCTTAAATATTGTATAT	5100
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DEFINITION	Human patched homology (PTC) mRNA, complete cds.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 6568) Hahn,H., Christiansen,J., Wicking,C., Zaphiropoulos,P.G., Chidambaram,A., Gerrard,B., Vorechovsky,I., Bale,A.E., Toflgard,R., Dean,M. and Wainwright,B.		
TITLE	A mammalian patched homology is expressed in target tissues of hedgehog and maps to a region associated with developmental abnormalities		
JOURNAL	J. Biol. Chem. 271 (21), 12125-12128 (1996)		
MEDLINE	96218118		
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AUTHORS	Hahn,H., Christiansen,J., Wicking,C., Zaphiropoulos,P.G., Chidambaram,A., Gerrard,B., Vorechovsky,I., Bale,A., Toflgard,R., Dean,M. and Wainwright,B.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-DEC-1995) Michael Dean, NCI-FCRDC, P.O. Box B, Frederick, MD 21702, USA		

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 Human homolog of patched, a candidate gene for the basal cell nevus
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 Science 272 (5268), 1668-1671 (1996)
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 Johnson, R. L., Rothman, A. L., Xie, J., Goodrich, L. V., Bare, J. W.,
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 Direct Submission
 Submitted (29-MAY-1996) Departments of Developmental Biology and
 Genetics, Howard Hughes Medical Institute Stanford University
 School of Medicine, Beckman Center B300, Stanford, CA 94305-5427,
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QY	2484	AGCCGAGAGAGCAGCAGCTCCACAAAGGAGCTGCTCTCCAGTTCTCCGACTCCAGCTC	2543
Db	2101	AGCCGAGAGAGCAGCAGCTCCACAAAGGAGCTGCTCTCCAGTTCTCCGACTCCAGCTC	2160
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QY	2604	GCTCCCTTCCTCTWTGAAACCAAAAGCCAAAGTGTGTGTATCTTCCTTTTCTGGGCTTG	2663
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QY	2664	CTGGGGGTCAGCCTTTATGAGCACACCCGAGTGAAGACGGGCTGACCTTTACGGACATT	2723
Db	2281	CTGGGGGTCAGCCTTTATGAGCACACCCGAGTGAAGACGGGCTGACCTTTACGGACATT	2340
QY	2724	GTAACCTCGGGAACCCAGACAAATATGACTTTATTTGTCGTCACAAATTCACTTTTCTTTC	2783
Db	2341	GTAACCTCGGGAACCCAGACAAATATGACTTTATTTGTCGTCACAAATTCACTTTTCTTTC	2400
QY	2784	TATCAACATGTATATATCTACGCCGGAAGAAGACATCCCGATATATCCAGACTTACTTTAC	2843
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QY	2844	GACCTATACAGAGAGTTTCAGTAACGTGAAGTATGTACTTTTGGAGAAACAAACACCTT	2903
Db	2461	GACCTATACAGAGAGTTTCAGTAACGTGAAGTATGTACTTTTGGAGAAACAAACACCTT	2520
QY	2904	CCCAAAATGTGCTGTCGACTACTTTCAGAGACTGCTTCAGGACTTCAGATGCACTTTTGAC	2963
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QY	3024	GTCCTGTGCTACAAACTCCTGTGTGTCAAAACCGGACGCGCATTAAGCCATTCAGATCAGC	3083
Db	2641	GTCCTGTGCTACAAACTCCTGTGTGTGTCAAAACCGGACGCGCATTAAGCCATTCAGATCAGC	2700
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QY	3144	ATCTACCTTACGGCTTTGGGTGCACCAACAGACCCCGTCGGTATGCTGCTCCCAAGCCACAC	3203
Db	2761	ATCTACCTTACGGCTTTGGGTGCACCAACAGACCCCGTCGGTATGCTGCTCCCAAGCCACAC	2820
QY	3204	ATTCGGGCAACACCGAGACAGAAATGGGTCCACGACAAACCCGACTCATGTGCTCGAAACAAG	3263
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QY	3264	CTGAGAAATCCCGGACAGACCCATCGAATATGCCAGTTCCCTTCTTACCTCAACGGG	3323
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QY	3324	TTTGGGGACAACCTCAGACTTTTGTGAGGGCAATTGAAAAAGTAAAGACCATTCGACGCAAC	3383
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Db	3001	TATPACAGGCTGGGGGTGTCCTCATTTACCCCAAGCGCTACCCCTTCCTTCTTGGAGAG	3060
QY	3444	TATCATGCGGCTCCGCACTGGTGTGCTGCTGTCACTACAGCGTGTGTGGCCCTGCACATTC	3503
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QY	3504	CTCTGTGCGCTGTCTTCTTCTTGTGAACCCCTGACGGCGGGATCATTTGTATGTCTCTG	3563

Db	3121	CTCGGTGCGCGTGTCTTCCTTCTGAAACCCCTGAGACGGCCGGATCATATTGATGATGTC	3180
QY	3564	GGCGTATGACGGTGGAGCTGTTCCGCAATGATGAGCCCTATCGGAATCAAGCTCAAGTGGC	3623
Db	3181	GGCGTATGACGGTGGAGCGTGTTCGGCAATGATGAGGCGCTATCGGAATCAAGCTCAAGTGGC	3240
QY	3624	GGCGCGGTGATCGTGTATCGCTTCTGTGGCATATGAGATGAGATTCACCCGTTCAAGTT	3683
Db	3241	GGCGCGGTGATCGTGTATCGCTTCTGTGGCATATGAGATGAGATTCACCCGTTCAAGT	3300
QY	3684	GCTTTGACCTTCTGACGGCCATTCGGCGACAAGAAACCGAGGGCTGTGTTGCCCTGGAG	3743
Db	3301	GCTTTGACCTTCTGACGGCCATTCGGCGACAAGAAACCGAGGGCTGTGTTGCCCTGGAG	3360
QY	3744	CACATGTTTGACACCCGTCCTGGATGAGCGCCGTGTCCATCTGCTGGAGTGTGATGCTG	3803
Db	3361	CACATGTTTGACACCCGTCCTGGATGAGCGCGGTGTCCATCTGCTGGAGTGTGATGCTG	3420
QY	3804	GGGGATCGATCGATGAGACTTCATTTGCAGGATTTCTTTGCTGTGCTGGCGGATCGTCACC	3863
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Db	3481	ATCCCTGGGGTCTCATATGGGCTGTGTTTGCTTCCGCTGGCTTTGCTTTCTTTGGACCA	3540
QY	3924	TATCCTGAGGTGTCTCCAGCCAACGGCTTGAAACGGCTGCGCCACACCCTCCCTGAGCCA	3983
Db	3541	TATCCTGAGGTGTCTCCAGCCAACGGCTTGAAACGGCTGCGCCACACCCTCCCTGAGCCA	3600
QY	3984	CCCCCAGGGTGTCCGCTTCCGCAATGCCGCCCGCGCCACACGACAGCGGGGTCTGATTC	4043
Db	3601	CCCCCAGGGTGTCCGCTTCCGCAATGCCGCCCGCGCCACACGACAGCGGGGTCTGATTC	3660
QY	4044	TCCGACTCGAGATATATGTTTCCAGACAGACAGTCTCAGGCGCTCAGCAGAGAGCTTCGGCAC	4103
Db	3661	TCCGACTCGAGATATATGTTTCCAGACAGACAGTCTCAGGCGCTCAGCAGAGAGCTTCGGCAC	3720
QY	4104	TACGAGGCCACAGGGCGCGGGAGGCGCTGCCACCAGTAGTCTGGAAGCCACAGAA	4163
Db	3721	TACGAGGCCACAGGGCGCGGGAGGCGCTGCCACCAGTAGTCTGGAAGCCACAGAA	3780
QY	4164	AACCCGCTTTCGCCCATCTCCATCTGTGTCTCATTCGGAAATCCAGGATTCACCCACCTCG	4223
Db	3781	AACCCGCTTTCGCCCATCTCCATCTGTGTCTCATTCGGAAATCCAGGATTCACCCACCTCG	3840
QY	4224	AACCCGAGACAGAGCCCAACCTCGAGTCAAGGATCCGCTCCGGACGGCAAGGCGCAG	4283
Db	3841	AACCCGAGACAGAGCCCAACCTCGAGTCAAGGATCCGCTCCGGACGGCAAGGCGCAG	3900
QY	4284	CAGCCCGAGAGGAGACCCCCCAAGAGAAGGCTTGCGCACCCCTTACAGACCGCGCAGA	4343
Db	3901	CAGCCCGAGAGGAGACCCCCCAAGAGAAGGCTTGCGCACCCCTTACAGACCGCGCAGA	3960
QY	4344	GACGCTTTGAAATTTCTACTGTAGAAGGCAATTCTGAGGCTTCTGAGCAATATGAGGCGCTGAGGC	4403
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Db	4021	CGTGGGGGGCCGCTCTCAACAACCCCGGAACCCAGCGTCCACTGCAATGGGAGCTCC	4080
QY	4464	GTCGCCGGTACTGCGCAGGCCATCACACTGTAGAGGCTTCTGCTCCGTAGACTGTGGCC	4523
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QY	4524	GTCGACCCGCCGCTGTCCCTGGGCGTGGGCGAACCCTCGAGGGGAGCTCTGCGCCAGCC	4583
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QY	4584	TATCCTGAGATCTACACAGGCGCTGTTTGAGAGACCCCAAGTGCCTTTCCAGATCCGATGT	4643
Db	4201	TATCCTGAGATCTACACAGGCGCTGTTTGAGAGACCCCAAGTGCCTTTCCAGATCCGATGT	4260

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 SOURCE
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 Unclassified.
 REFERENCE 1 (bases 1 to 5187)
 AUTHORS Scott, M.P., Goodrich, L.V. and Johnson, R.L.
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 JOURNAL Patent: US 5837538-A 3 17-NOV-1998;
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 QY 1106 ACAGCTGGGACGATACCTCTGTTGATTAATTACACCTTTGGACTCTTGTGGAAAGGGCGAAAGCT 1165
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QY	2126	GGTTCATATTTTGGCATGGTCTCTGTCATTTTTCCTGCAATTCAGATGGATTTATA	2185
Db	1797	GGATTTTCAATTTTGGTATGGTTCTCTCAATTTTCTCGAATTTTCAGATGGATTTATA	1856
QY	2186	TCGACGCAAGACAGAGAGACTGGATATTTTTCGTGTTTACAAAGCCCTGGCTCAGAG	2245
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QY	2246	AGTGAATCAGGTTGAACTTCAGAGCCTACACGACACACAGCAATACCGGTCAAGCCC	2305
Db	1917	GGTGAATCAGATTGAGCCACAGGCTTACACAGCCTCAGATMAACCCGGTACAGCCC	1976
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Db	2037	CCTTACAGCTCCCGACAGAGATATGAGCCCTCACAGCAGGTACTACACACCGCCGAGACC	2096
QY	2426	GGCGTCCGAGATCTCTGTGACGCCGCTCAACCGTGAACACAGAGACACCTCAGCTGCAGAG	2485
Db	2097	ACGCTCTGAGATCTCTGTACAGCCTGTACCGTCAACCGACAGCAACCTCAGCTGTACAG	2156
QY	2486	CCCAGAGACACAGAGTCCACAAAGGAGACCTGCTCCAGTTCTCGAGATCCAGCCCTCA	2545
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QY	2606	TCTTTTCTCTTTGAAACCAAAAGCCAAAGTAGTGATCTTCTCTTTTCTGGGCTTGCT	2665
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QY	2846	CTTACACAGAGAGTTTACGTAAACCTGAAGTGTGCATTTTGGAGAAACAAACAGCTTCC	2905
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QY	2966	TGACTGTGGGAACCGGGGAAATCATGCCAAACATTTACAAATATGATCAAGACATGGAGT	3025
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QY	3026	CTTGGCTTCAAACTCTGGTGTGAAACCCGAGCCGCGGATTAAGCCATTCGACATCAACCA	3085
Db	2697	CCTCGCTTACAACTCTGTGTGAGACTGACAGCTGACGCCGAGACAAAGCCCATTCGACATTA	2756
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QY	3266	GAGAAATCCCGGAGAGAGAGCCCATGAGATGCCAGTTCCCTTTCTACCTCAACGGGTTT	3325
Db	2937	GAGATATCCAGACAGAGACCCCATGAGTACGTCAGTTCCCTTCTTACTCTCAACGGGCT	2996
QY	3326	GGGGACACCTTAGACTTTTGTGAGGCAATTGAAAAAGTAAAGACCATCTCGACGAACATA	3385
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QY	3446	CATGGCGCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGTGTTGGCTGACATTTCT	3505
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QY	3506	CGTGGCGCTGTGCTTCCCTCTGTAACCCCTGGAGCGGGCGGGATATTGTGTATGGTCCGGC	3565
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QY	3986	CCCCAGCGGTGTCCGTTTGGCATATGCCGCCCGGCGCACAGCGGGGTCTGATTTCTC	4045
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Oy 5109 ATAAATCTGATGAAATATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 5168
Db 4766 ATAAATCTGATGAAATATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4824
Oy 5169 ATATTTTAAATTTGATATCAACACCTGCTGATGATGATGATGATGATGATGATGATGAT 5228
Db 4825 ATATTTTAAATTTGATATCAACACCTGCTGATGATGATGATGATGATGATGATGATGAT 4884
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Db 4885 AACACGCTATGCTGATATTTTGTGTTTAAATGACGATATGAAGAAAC 4931

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RESULT 5
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 LOCUS AR055791 5187 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 9 from patent US 5837538.
 ACCESSION AR055791

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VERSION AR055791.1 GI:5981368
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5187)
AUTHORS Scott, M.P., Goodrich, L.V., and Johnson, R.L.
TITLE Patched genes and their use
JOURNAL Patent: US 5837538-A 9 17-NOV-1998;
FEATURES
    source
        location/Qualifiers
            1..5187
BASE COUNT 1165 a 1412 c 1337 g 1270 t 3 others
ORIGIN
Query Match 71.9%; Score 3801.2; DB 81; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;
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[illegible]

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Db	2037	CGTTCAGCTCCGCACAGAGTATGAAACCTTCACACGCAGCTGTACTACACACCGCCGAGCC	2098
Qy	2426	CGCGTCCGAGATCTCTGTGACAGCCCTTCACCGTGCACACAGACACCTTCAGCTCCGACAG	2485
Db	2097	ACGCTGTGAGATCTCTGTACAGCCTGTATTACCGTACCCAGGACAAACCTCACGCTGTACAG	2156
Qy	2486	CCGAGAGAGCACACGACTCCACAAAGGACCTCTCCCGAGTTCCTCCGCTCCGACCTCCACA	2545
Db	2157	TCCGAGAGAGCACACAGCTCTACACAGGACACTCTCTCCAGTTCCTCAGCTCCAGCTCCACA	2216
Qy	2546	CTGCTCTGAGCCCCCTCTGTACGAAGTGCACCTCTATCTTTTCTGTGAGAGCACTATGC	2605
Db	2217	CTGCTCTGAGCCCCCTCTGCACCAAGTGCACCTCTCTCTGTTGACAGAGCACTATATGC	2276
Qy	2606	TCCCTTCTCTGTGAACCAAAAGCCAGAGTATGATCTTCTCTTTTCTGTGGCTTGTCT	2655
Db	2277	TCTTTTCTCTCTGTGAACCCCAAGCCAAAGTGTGTATCTCTTTTCTGTGGCTTGTCT	2338
Qy	2666	GGGGGTACGCTTTTATGTGACACACCCAGTAGAGAGAGGGCTGCAGCTTACGACATATGT	2725
Db	2337	GGGGGTACGCTTTTATGTGAGACCCGAGTGTGAGAGAGGGCTGTGACCTTCACGACATTTGT	2386
Qy	2726	ACCTCGGGAAACCAAGAAATATGACTTTATTTGCTGCACAAATTCATTAATCTTTCTTCTTA	2785
Db	2397	TCCCGGGGAAACCAAGAAATATGACTTTATATGCTGCCAGCTTCAAGTACTCTCTTCTTA	2456
Qy	2786	CAACATGTATATAGTACACCCAGAAAGCAGACTACCCGCAATATCCAGACACTTACTTACGA	2845
Db	2457	CAACATGTATATAGTACCCAGAAAGCAGACTACCCCAATATCCAGACACTTACTTACGA	2516
Qy	2846	CCTACACAGAGATTTCATGTAACGTGAAGTATGTCATGTTGGAGAGAAACCAACAGCTTCC	2905
Db	2517	CCCTTCATTAAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGAGAAACAGCAACTTCC	2576
Qy	2906	CAAAATGTGCTGCACACTACTTCAGAGACCTGGCTCAGAGGACTTCAGAGTATGATTGACAG	2965
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Qy	2966	TGACTGTGGAAACCCGGGAAATTCATGCCAAACATTTACAAAGATGATCAGACATGTAGAT	3025
Db	2637	TGACTGTGGAAACCTGGTGAGACTGTGCAGCCGAGCAAGCCCATTCACATTAATGTCA	2696
Qy	3026	CCCTTGCGCTACAAACTCTCTGTGTGCAAAACCGGACGCGCGATTAAGCCATTCGACATCAGCCA	3085
Db	2697	CCCTTGCGCTACAAACTCTCTGTGTGAGACTGTGCAGCCGAGCAAGCCCATTCACATTAATGTCA	2756
Qy	3086	GTTGACTTAACACACGCTGTGTGTGATGAGATGAGATATTAATCCGAGGCTTTCTTCAT	3145
Db	2757	GTTGACTTAACACACGCTGTGTGTGAGACTGTGCAGCCGAGCAAGCCCATTCACATTAATGTCA	2816
Qy	3146	CTTACTGACGGCTTGGGTGACGACGACCCCGTGCCTATGTGCTGCCCTCCAGGCGCAACAT	3205
Db	2817	CTTACTGACGGCTTGGGTGACGACGACCCCTGTATGCTTACGTGCTGCCCTCCAGGCGCAACAT	2876
Qy	3206	CCGGCCACACCGGACCAAGATGGGTCCACGCAAAAGCCGATACATGCTGTAAACAGGCT	3265
Db	2877	CCGGCCCTCACCGGCGGAGTGGGTCCATGTGCAAAAGCCGATACATGTCACAGACAGGCT	2936
Qy	3266	GAGATATCCGGGACGAGAGCCCATGTGAGTATGCCCAGTTCCCTTCTTACCTCAACGGGTT	3325
Db	2937	GAGATATCCGAGCGAGAGCCCATGTGAGTATGCGCTACGCTTCCCTTCTTACCTCAACGGCT	2996
Qy	3326	GGGGGACACTCAGACTTTTGTGGAGGCAATTTGAAAAAGTAAAGACCATCTGCGCAACTTA	3385
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Qy	3386	TACGAGCCTGTGGGCTGTCCAGTTATCCCAAGCGCTACCCCTTCTCTTCTGGGAGCAGTA	3445
Db	3057	TACGAGCCTGTGGGCTGTCCAGCTTATCCAGCTACCCCAATGCTACCTCTTCTTCTGGGAGCAGTA	3116

QY	3446	CAGGGCCGCGCCACTGGCTGCTGCTGTTCAATCACAGTGGATTGGACCTGCACATTCCT	3505
Db	3117	CATCACGCTCGCCCACTGGCTCTGCTGTATTCATCACGCTGGTGTGGCTGCACGTTTCT	3176
QY	3506	CGTGTGCGCTGTCTTCTCTTCTGTGAAACCCCTGGACGGCGGGGATCATTTGTATGTCTGGC	3565
Db	3177	AGTGTGGCAGCTTCTCTCTCTGAACCCCTGGAGCGCGGGATCATTTGTCAATGTGCTCGGC	3236
QY	3566	GCTGATGACGGTCGAGCGCTGTGGCATGTATGGGCCCTCATCGAATCAAGCTCAAGTGGCGT	3625
Db	3237	TCTGATGACCGTTGAGCTCTTTGGCATGGATGGGCTCTATTTGGATCAAGCTGATGCTGT	3296
QY	3626	GCCCTGTGTCATCCCGATGCTCTTGTGGCATAGGATGGAGATTCACCGTCAAGCTTGC	3685
Db	3297	GCCTGTGGTCATCTGATTTGCAATCTGTGTGGCATCGGAGTGGATTCACCGTCAAGCTTGC	3356
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QY	3866	CCGTGGCGCTTTCATGAGGCTGGTTTGTGTCCCGTGTCTTGTCTTTCTTTTGGACATA	3925
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QY	4046	CGACTCGAGTATAGTTCCACAGACAGATGTGAGGCTTCAGCGAGGAGCTTCGGCACTA	4105
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QY	4106	CGAGCGCCACAGAGGGCGGAGGCCCTGTGCCACCAAGTATGCTGTGAAGCCACAGAAAA	4165
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QY	4406	TGCGGGGGCGCGTTTTCACAACTCTGGAAACCAAGGTTCACTGCAATGGGCACTCGCT	4465
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OY	4526	GCACCCGGCGGCTGTCCCTTCGAGGCTGGGGGGGAACCCCCGAGGGGGACTGTGGCCAA- ---	4581
Dd	4197	GCATCCCCC-----CCTGAGACTGTGGGCGCAACCCCAGGGGGGCCCTGTGCACAGCTTA	4250
OY	4582	----GCTAACCTGAGACTGACCACGGGCTGTTTGAGAGACCCCCACGTCCTTTCACAGT	4636
Dd	4251	TGAGAGCTACCTGTAGAGACTGATCACGGGGATTATTTGGAGTTCCTCATGTCCCTTTCATGT	4310
OY	4657	CCGGTGTAGAGAGAGGATTGGAAGGTGGAACATGAGCTGCGACAGAGCTGGAAATGGCA	4696
Dd	4311	CAGGTGTAGAGAGAGGACTCAAAGTGTGAGTCAATAGACTACAGACACTGGAAATGTGA	4370
OY	4697	GGAGAGGCCCGGGGAAAGCAGCTCCAACTGAGGGTGAATTAATCTGAAGCAAAAGGCC	4756
Dd	4371	GGAGAGGCCCGTGGGGAGGACGACTCCAACTAGGGGTAAATTAATCTGAGACAAGAAGGCC	4430
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Dd	4531	TGATTTTKGGGAATAATTTCTATATAAATTTTAAAGGTGTACACA--TGTAATATTAATGTG	4588
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OY	5169	ATATTTTAATTTGCAATTCACAGCAACCGCTGGTAGTAGTAAGAAATGTTACTGTTAACTTTCA	5228
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OY	5229	AACACGCTATGCGTGTAAATTTTTTTGTTTAAATGAGCAGATATGAGAAAGC	5280
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LOCUS	MMU46155		
DEFINITION	MMU46155	4305 bp mRNA	ROD
ACCESSION	U46155	Mus musculus patched mRNA, complete cds.	31-DEC-1998
VERSION	U46155.1	GI:1181884	
KEYWORDS			
SOURCE		house mouse.	
ORGANISM		Mus musculus	
REFERENCE		Murakami; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE		Goodrich,L.V., Johnson,R.L., Milenkovic,L., McMahon,J.A. and	
JOURNAL		Conservation of the hedgehog/patched signaling pathway from flies	
MEDLINE		to mice: Induction of a mouse patched gene by Hedgehog	
REFERENCE		Genes Dev. 10 (3), 301-312 (1996)	
AUTHORS		2 (bases 1 to 4305)	
		Scott,M.P.	

TITLE Direct Submission
JOURNAL Submitted (18-JAN-1996) Matthew P. Scott, Departments of

Db 1041 AACGATGTCACAGTTAAAGACTCCCAAGCAAAATGATGAACACTTTCAGGGGCTACGACTA 1100
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Db 3021 CATGCGCTCCGCGCAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3080
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Db 3141 TCTGATGAGCAGTGTGAGAGTCTTGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3200
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Db	62	GCACCGCGGCGCGCGCGACGACCCCGTTTCGGCGGCGAGGAGTGCCTCGCGCGCGCGCG	121
Qy	484	GACGCAACGGGGGGGCTGCGCCCGTGTGTGCGCGCGCGGACCGGGAGCTATCTGCACCGCGCCA	543
Db	122	GGCGGAGCGGAGGAGACCCGCGCGCGCGCGCGCGCGCGGAGTACTCAGCGGCGCGA	181
Qy	544	GCTACTGCGACGCGCGCGCTTCGCTCTGAGAGAGATTTTCAAGGGGAGAGGCTACTGGCGCGA	603
Db	182	GCTACTGCGCATGCGCGGCTTCGCTTGTGAGAGAGATCCGAAAGCGGACGACTACCGGAGGA	241
Qy	604	AAGCGCACTGTGGCTGTAGAGCGAGATTTTCAGAGACTCTTATTTAACTGAGTGTTTACA	663
Db	242	GAGCGCGCGTGTGTGCGGAGCGAATTTTCAGAGACTGCTCTTTAACTGGGCGTGTACA	301
Qy	664	TTCAAAAAAACTTCGCGCAAGTTTGTGGTGTGGGCGCTCCTCATATTTGGGCGCTTCGCGG	723
Db	302	TTTCAGAAAACTCGCGCAAGTTCTCGTGTGCGCGCTGC--TATATTCGCGGTTCGCGG	358
Qy	724	TGGGATTAAGAGGAGCAACCTCGAGCCCAAGCTGGAGGAGCTGGGGTGGAAATTGGAG	783
Db	359	TGGGATACCGCGCGCGCAACTAGAACCACTAGAGGAGCTGTGGGTGGAACTGTGTG	418
Qy	784	GACGAGTAAGTGTGTGATTTAAATTAATTAATCTGCGCAGAAATTTGAGAGAGGCTATGTTTA	843
Db	419	GACAGTGTAGTGTGGAGTTAAACTACACACGCGAGAAATTTGGAGAGAGGCCATGTTTA	478
Qy	844	ATTCCTCACTCATGATACAGACCCCTTAAGAGAGAGGTGCTAATGTCTGACACAGAG	903
Db	479	ACCCCGCGCTCATGATTCAGACTCCACAGAGAAATGGAATTAATGTCTCAACAAGAG	538
Qy	904	CGCTCTCAACAACCGTGGACTGGGCACTCCAGGCGAGCGGTGTCAATGTATACATGTACA	963
Db	539	CACCTCGGAGCACTTGTGACTGTGCACCTTCAGGCGACGACAGATCATGTTTATATGTACA	598
Qy	964	ACAGGCACTGAAATTTGGAACATTTGTGTACAAATCAGAGAGCTTATACAGAAACAG	1023
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Qy	1024	GTTTACATGATCAGATTAATAGAAATATCTTTAACCTTGTGTTGATTAATACACTTTGGACT	1083
Db	659	GCTATATGAGCAAGATTATAGAAATACCTTTATCTTGTCTAAATTAATACCTTTGGACT	718
Qy	1084	GCTTCTGGGAGGGGGAATTCACATCTGGGAGAGATATACCTCTCTGATGTAACCTCTCT	1143
Db	719	GCTTCTGGGAGGAGCAAAAGCTACAGTCTGGAACTGCTTATCTATTTAGGAGAGCTCTCT	778
Qy	1144	TGCGGTGACAAACTTCGACCCCTTTTGGAAATCCTGTGAAGAATTAAAGAAAATAAATCATC	1203
Db	779	TGCGAGTGCATCAACTTTGACCCCTTATGAAATTTCTTGGAGAAGTTTAAAGAAAATAAATCATC	838
Qy	1204	AAGTGCACAGCTGTGGAGGAAATGCTGAATTAAGGCTGAGTTGTCATGTTTACATGGACC	1263
Db	839	AAGTGCAGAGCTGTGGAGGAAATGCTGAATTAAGGAGGTTGGTCACTGTTTATATGATC	898
Qy	1264	GGCCCGGCTCAATCCGGGCGAATCCAGACTGCGCCCGCACAGCCCGCAACAAAAATTGCA	1323
Db	899	GACCTTGGCTGAATCCTGTGATCTCGATTTCCATGAGCTCCCAATCAAGCTCCCAATTAATTTCTA	958
Qy	1324	CCAAACCTTTATATATAGCCCTTGTGTTTGAATGGTGAATCTACAGGCTTATCCAGAAAGT	1383
Db	1019	ACATGATTTGGCAGAGAAAGTTAATATATATAGTGTACAGTCAAGAAACAGTTCTGTGTAAC	1078
Qy	1444	TGCTAGAGCCCATGCGCTGCGAGACCATGTTCCAGTTAATGACTCCCAAGCAATGTACG	1503
Db	1079	TTGTGTAGTCCACAGGCTTTTGCAAAACCATGTTCAGTTTAATAGCTCTCAACCAATGTATG	1138

QY	1504	AGACTTCAAGGGGTACAGATATGTCTCACACATCAACTGACGAGGACAAAGCGGAC	1503
Db	1139	ACCACTTCAAGGGATATGAAATATGTTTCACTATCAACTGGAATGAGGAATAAAGCACAG	1198
QY	1564	CCATCTCGAAGCGCTCGCAGAGAGACATATATGAGAGGTGCTTCAATCAGATGTCCACAGA	1632
Db	1199	CAATTCGTGAAGCTCGCAGAGAGATGTATGTCCAGGTGTTCATCAAAAGTGTTCACAAA	1258
QY	1624	ACTCCACTCAAAAGTGTCTTCTCTTACACACACAGACCTTGAGGACATCCTGAAATCCT	1683
Db	1259	ACTCTACTCAGAAGGGGTCTTCTCTTACTACTCAACTACCTCGGAGACATCCTAAAGTCAT	1318
QY	1684	TCCTACGCTCAGTGTCACTCCGGGTGGCGGCGGATCTTACATCACTCTGGCCATGAGCT	1743
Db	1319	TTTTCTGATGTCACTGTTATTCAGAGTACGTAGTGGCTACTTACTATATCTTGCCATCGCT	1378
QY	1744	GCTCAACACTGCTCCGCTGGGACTGCTCCCAAGTCCAGGGTGCCTGGGCTGGCTGGCG	1803
Db	1379	GTTTAAACATGCTGAGGTGGGATTTGTTGCCAAAGTCTCAAGGTGCCGTGGGTGGCAGAG	1438
QY	1804	TCCTGTGGTGTGACTGTCAGTGGCTGCGAGGACTGGGCTGTGCTCATTTGATGGAAATTT	1863
Db	1439	TCCTGTTGGTGTGACGTGACGTAGTGGCTCGACAGCTTGGGTCTGTGCTCACTAATGGAAATTT	1498
QY	1864	CCCTTAAACCTGCAACAACTCAGGTTTTTGGCATTTTTCGCTCTTGAGTGTGTGATGATG	1923
Db	1499	CCTTTATATGCTGCAACACTCAGGTTCTGCTTTTCTGTCTTCGGAGTTGGTGTAAATG	1558
QY	1924	ATGTGTTTTCTGTGGCCCAAGCCCTTGAGTGAACACAGGACAGAAATAAAGAAATCCCTTTTG	1983
Db	1559	ATGTTTTCTCTGTAGCCCAATGCGCTTATGTTGAACACAGACAGAAATAAGAAATTCATTTTCG	1618
QY	1984	AGGACAGGACCGGGGGGTGGCTCTAAAGGACAGAGGACAGCGGGCCCTCAGCTCATCA	2043
Db	1619	AGGACAGAACAGGTGATGTTTAAAGCGAAGAGAGCAATGTAGCCCTTACATCTATCA	1678
QY	2044	GCAATGTCAGAGCTTCTTCATGGCCGCGTTAATCCCAATTCGCCCTCTCGGGCGTTCT	2103
Db	1679	GCAATGTACTGATCTTTATGTGGTGCCTTAATCCCTATCTTCGTTACGACATTTT	1738
QY	2104	CCCTCAGGACGGGTAGTATGCTGTGTCAATTTTGGCATAGTGTCTCATTTTTCCTG	2153
Db	1739	CACCTCAAGCAGAGTGTGGTATGATTCACATTTTGGAAAGTGTCTCTAATTTTTCCTG	1789
QY	2164	CAATTCACAGATGATTTATATCGAGCGCAGAGACAGGAAGCTGGAATTTTTCGTGT	2232
Db	1799	CTATACTGAGCATGGACCTTTATCGTGGAGAGACAGAGACATGGAAATATTCTGCTGT	1858
QY	2224	TTTACAAGCCCCGTGCTCAGCAGAGTATTTAGGTTGAACCTCAGGCTTACACCGACACAC	2283
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QY	2284	ACGACAATTCACGGCTCAGCGCCCCCAACCTCCCTTACAGACCCACAGTTTGGCCATGAA	2343
Db	1916	ATGACATATTTTGTTCACAGTCTTCACACCCCGCTACAGCAATCAGATTTTGGACATGAA	1975
QY	2344	CGCAGATTACATGACGTCACTGTCCAGCTCCGACAGGATACGAGCCCCACAGCGAGC	2403
Db	1976	CTCAGATTTCAAATGACGTCTTACAGTCCAGTTGGCGACCTGAATTTGATCTCTATACAAAG	2035
QY	2404	TTTACTACACACCGGTGAGCGCGCGTCGAGATTCCTGTGACGCGGTTCACCGTGCACAC	2463
Db	2036	CGTACTACACCACTGAGAGCCACGATCGAATAATTCATAGTACAGCCTGTGACAGTGACTC	2095
QY	2464	AGGACACCCCTCAGCTGCGCAGAGCCACAGAGACACAGACTTCACAGAGGACCTGTCTGCC	2533
Db	2096	AAGATATGCTTATGCTGCCAAAGGCCAGAAAGCCCAAGCTCAACAAAGGAAATTTGCTTTCC	2155
QY	2524	AGTTCTCGAGTCCAGCTTCACATGCTGTGAGCGCCCTGTACAGATGAGACACTCTCAT	2583
Db	2156	AGTTCTCGAGTTCACATGCTGTGCAATTTGCTTGAAGCCACCTGTGTACGAAGTGGACACTCTCAA	2215

QY	2584	CTTTGGCTGAGAAACGACATATGCTCTTTCTCTTTGAAACCAAAAGCCAAAGTACTGCTGA	2643
Db	2216	CTTTTGAGAGAAAAACATTAATGCTCCGTTCCCTCTTAAACCAAAAGCTAAGTTGTGGTTA	2275
QY	2644	TCCTCCCTTTTTCGCGGCTCTGCGGGGTGACGCTTTATGGACACCAGCTGGTAGACAG	2703
Db	2276	TTTTTCTTTTCTTGCGGCTTACTTTGGGCTCAGCCTCTATGGAACACTACCAGGCTGAGAAATG	2335
QY	2704	GCGTGAACCTTACGAGCAATTTGACTCTGGGAAACACAGAGAAATATGACTTTATTTCTGCAC	2763
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QY	2764	AATTCAATATCTTTTCTTTTACAAACATGATATAGTCACCCAGAAAGCAGACTACCCGA	2823
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QY	2824	ATATCCAGCACTACTTTACGACCTACACAGAGTTTCACTAAGTGAACATATGCTATGT	2883
Db	2456	ATATCCAGCACTACTTTACGAACTTACAGAAAGTTTACACAATGTACATATATGTTTTGT	2515
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QY	3244	ACTACATGCGCTGAACAAAGGCTGAGATCCCGGACAGAGAGCCCATGAGTATGCCAGT	3303
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QY	3364	TAAAGACATCTGACAGCACTATACAGGCTGGGGGTGTGCCATTTACCCCAACGGGCTAC	3423
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QY	3424	CCTTCCTCTTGGGAGCAGTACATGGGCTCGGCCACTGGCTGCTGCTTTATCATAGCG	3483
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Db	3416	TTCTTGGAGTGTATATGCTTGCAGAGATCAAGATTTGATTTATTTATGTCAAGTAATTTCTTGG	3472
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Db 4364 GAAGAGAGGCGCAAGATTGAACTGTTTTCAGAGAACTGCTGGAAAAGAACTTGC 4423

OY 4804 GAGAACTGTTGGA 4817

Db 4424 CCGACATTGTTAGA 4437

RESULT 8

DRE007742 3732 bp mRNA VRT 24-MAR-1999

LOCUS Dario rerio mRNA for patched-2 protein.

DEFINITION A007742.1 GI:4539023

ACCESSION A007742.1

VERSION patched-2 protein; PTC1.

KEYWORDS patched-2 protein; PTC1.

SOURCE zebrafish.

ORGANISM Dario rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidae; Cyprinidae; Rasbora; Dario.

REFERENCE 1 (bases 1 to 3732)

AUTHORS Lewis, K.E., Concordet, J.P. and Ingham, P.W.

TITLE Characterisation of the second ptc gene in zebrafish

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3732)

AUTHORS Lewis, K.E.

TITLE Direct Submission

JOURNAL Submitted (21-AUG-1998) Lewis K.E., Developmental Genetics, Krebs Institute, Developmental Genetics, Krebs Institute, Firth Court, Western Bank, Sheffield S10 2TN, UK

FEATURES

source

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Db 88 CGACCGCCCGCGCGGATTTTGAGATTTTGCAGCGCGCGGACTATTTGGGATTCGCTTTT 147

OY 564 GCTTGGAGCAGATTTTCCAGAGGAGCTTACTGCGCCGAAAGCCCACTGTGGCTGAGA 623

Db 148 GCGCTGGAGCAGATTCAGAGGAGATGCGCTGGAGGAAAGCCGCTGTGGTTGAGA 207

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OY 804 AATTATCTGCGCCGAGAGATTGAGAGAGAGCTATGTTTAACTCTCACTCATGATACAG 863

Db 388 AAGTACACACGCGCAGAAATGCGAGAGAGAGAGGCACTTGTAGCTCTACCTCATGATACAG 447

OY 864 ACCCTTAAGAGAGAGGTGCTATATGCTGACACAGAGCGCTCTACAACTCTGAGC 923

Db 448 ACCGCTGTGAGAGAGGCTTAACATTTTGACCCGACGCGCTTAACGACGACCTGAC 507

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OY 1344 CTTGTTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1403

Db 928 CTTGTTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987

OY 1404 TTGATTTGGGTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1463

Db 988 CTTATCTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047

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OY 1584 AGGACATATGTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1643

Query Match 37.2%; Score 1965; DB 4; length 3732;

Best Local Similarity 72.5%; Pred. No. 7.8e-287;

Matches 2637; Conservative 0; Mismatches 895; Indels 105; Gaps 3;

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 Db 865 ACCTTACCTTGGTTAATCATATACACCTTTGGACTGCTTCGGGAGAGGGCAATTTAC 924
 Qy 1108 ACTGCGGAGACGATACCTTCTAGTAAACCTCTTGGCGGTGACAACTTGCAGCCCTT 1167
 Db 925 ACTCGGAGACGATACCTTCTAGTAAACCTCTTGGCGGTGACAACTTGCAGCCCTT 984
 Qy 1168 TGAATTTCTGAGAGATTAAGAAATTAACATATCAGAGGAGACAGTGGGAGAAATTC 1227
 Db 985 TGAATTTCTGAGAGATTAAGAAATTAACATATCAGAGGAGACAGTGGGAGAAATTC 1044
 Qy 1228 TGAATTAAGGCTAGGTTGTCATGTTACATGAGACCGCCCTCTCAATCCGGCCGATC 1287
 Db 1045 TGAATTAAGGCTAGGTTGTCATGTTACATGAGACCGCCCTCTCAATCCGGCCGATC 1104
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 Db 1645 CTGACAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1704
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 Db 1705 TTTTGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
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 Qy 2068 CCGCGTAAATCCCAATTCGCGCTGCTGCGGGGCTTCTCCCTCAGGAGCGCTAGTAGTG 2127
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Qy 2128 TCTTCAATTTTCCAGATGCTTCTGCTCATTTTCTCCGCAATTCCTCAGCATGATTTATATC 2187
 Db 1945 TATTTCAATTTTCCAGATGCTTCTGCTCATTTTCTCCGCAATTCCTCAGCATGATTTATAC 2004
 Qy 2188 GACCGGAGACGAGACGATATTTTCTGCTTTCAGAGCCCTCGCTCAGCAGAG 2247
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 Qy 2248 TG 2249
 Db 2065 TG 2066
 RESULT 10
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 ACCESSION X98883
 VERSION X98883.1 GI:1524009
 KEYWORDS patched protein; ptc1 gene.
 SOURCE zebrafish.
 ORGANISM Danio rerio.
 Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.
 REFERENCE
 AUTHORS Concorde, J.P., Lewis, K.E., Moore, J.W., Goodrich, L.V., Johnson, R.L., Scott, M.P., and Ingham, P.W.
 TITLE Spatial regulation of a zebrafish patched homologue reflects the roles of sonic hedgehog and protein kinase A in neural tube and somit patterning
 JOURNAL Development 122 (9), 2835-2846 (1996)
 MEDLINE 96379744
 REFERENCE 2 (bases 1 to 3672)
 AUTHORS Lewis, K.E.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUN-1996) K.E. Lewis, Imperial Cancer Research Fund, MOE, Room 408, ICRF, 44 Lincoln Inn Fields, London, WC2A, UK
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Query Match 25.88; Score 1362.2; DB 4; Length 3672;
 Best Local Similarity 62.9%; Pred. No. 5e-196;
 Matches 2244; Conservative 0; Mismatches 1278; Indels 45; Gaps 7;

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 QY 566 TCTGAGACATTTCCAAAGGAGGAGCTACGCGGAGGCGGAGGCGGCTGAGAGC 625
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 QY 626 GAAGTTTCAGAGACTCTTATTTAACTGGTTTACATTCACAAAAAAGCTGCGGCAATT 685
 DB 195 GAGGTTCCAGGCTTCTCTTCTCTGCGCTGTCACATCCAGGACACTGTGGAAAAAGT 254
 QY 686 CTTGTTGTGGGCTCTCATATTTGGGCGCTTGGCGGTGGATTTAAAGAGCGAGCT 745
 DB 255 GCTTTTATTTGAGCTCTTGTGTTGCGAGCGCTGTCTGTGGGTTGGCGGTGCTGCCAT 314
 QY 746 CGAGACCAAGCTGGAGAGCTGTGGTGGAGATTGGAGAGAGAGTAACTCGTAATTAA 805
 DB 315 TGAACGAGACTATAGAGAACTATGAGTGGAGAGAGAGAGAGAGAGAGAGAGTACG 374
 QY 806 TTTATCTGCGCAGAGATTGAGAGAGAGCTATGTTTAACTCTCACTCATATACAGAC 865
 DB 375 CTACACAAAAAGAGAGAGAGAGAGAGAGAGTCACTCACTCACTCATATACAAAC 434
 QY 866 CCCAAAGAGAGAGAGTGTATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 925
 DB 435 ACCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
 QY 926 GGCATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
 DB 495 AGCTCTGACAGCTAGCAAGAGTCAAGTGTCTTATGAGAAATCTTGGAGTCTTAATA 554
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 DB 555 AATATGCTTCAATCTGAGAGTTCATATATAGAAATGTCATGATGAAAGAGATGATA 614
 QY 1046 ATATCTTACCTGTTTATATATATACAGCTTGGAGCTCTCTGAGAGAGAGAGAGAT 1105
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 QY 1346 TGTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1405

DB 912 TGAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
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 DB 1806 GGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1862
 QY 2306 CCGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365
 DB 1863 TCCAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1922
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Db 1983 CACCTCCAGATATCCACCACTCTCCATCCATGCTCTATCCACACCAACCCCTTACAC 2042
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RESULT 11

AF091501

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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 ORIGIN

Query Match 22.2%, Score 1176.4; DB 10; Length 3612;

Best Local Similarity 61.5%; Pred. No. 4.8e-168;

Matches 2058; Conservative 0; Mismatches 1221; Indels 69; Gaps 8;

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 DB 139 CTGGGATGCGGGATTCAGAGACATGTGGCAAGTCTTCTTGAGACTGTTGGCTTT 198
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 DB 199 GGGGCTTCGCGGTGGGATTAAAGACAGCACTTCGAGACCAAGCTGGAGAGCTGTG 258
 QY 771 GTGAGAGTTGGAGAGCAATGATGATTAATTTATCTCGGCAAGATTAAGTGAAGA 830
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 DB 319 GAGGCTGATACCTCTCAAGATGCTGATACAGACCGCAGCAGAGAGAGAGACATC 378
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 DB 379 CTCACACCGGAGAGCACTTGCCCTCCAGCAGCGCCCTCACTGCGAATAAGTCCAA 438
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 DB 439 GTATACATGTGAAGTCTCGGGAATTTGAACAAATCTGCTACAGACGAGAGTCCG 498
 QY 1011 ATCAGAGAACAGTTTACATGATGATTAATAGAAATCTTTACCCTTTGTTGATTAT 1070
 DB 499 CTATTGTAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATG 558
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VERSION AF119569.1 GI:4325110
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
Tollgard,R.
TITLE A novel human patched gene, undergoing alternative splicing
and up-regulated in basal cell carcinomas
JOURNAL Cancer Res. 59 (4), 787-792 (1999)
MEDLINE 99151521
AUTHORS
TITILE Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
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JOURNAL Direct Submission
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Sweden
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 REFERENCE 1 (bases 1 to 3612)
 Smeyth, I., Narang, M.A., Evans, T., Heilmann, C., Nakamura, Y.,
 Chenevix-Trench, G., Pletsch, T., Wicking, C. and Mainwright, B. J.
 Isolation and characterization of human patched 2 (PTCH2), a
 putative tumour suppressor gene in basal cell carcinoma and
 medulloblastoma on chromosome 1p32
 Hum. Mol. Genet. 8 (2), 291-297 (1999)
 JOURNAL Hum. Mol. Genet. 8 (2), 291-297 (1999)
 MEDLINE 99135908
 TITLE 2 (bases 1 to 3612)
 AUTHORS Smeyth, I., Narang, M.A., Evans, T., Heilmann, C., Nakamura, Y.,
 Chenevix-Trench, G., Pletsch, T., Wicking, C. and Mainwright, B. J.
 DIRECT SUBMISSION
 JOURNAL Submitted (28-AUG-1998) Center for Molecular and Cellular Biology,
 University of Queensland, Ritchie Laboratories, Research Rd.,
 Brisbane, QLD 4072, Australia
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AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
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JOURNAL	Takabatake,T.		
Direct Submission			
Submitted (04-FEB-1998)			
to the DBJ/EMBL/GenBank databases.			
Takabatake, Nagoya University, Radioisotope Research Center;			
Furuta-cho, Chikusa, Nagoya, Aichi 464-8602, Japan			
(E-mail:145998@nuc.cc.nagoya-u.ac.jp, Tel:052-789-2573,			
Fax:052-789-2567)			
2 (sites)			
Takabatake,T., Ogawa,M., Takahashi,T.C., Mizuno,M., Okamoto,M. and			
Takeshima,K.			
Hedgehog and patched gene expression in adult ocular tissues			
FEBS Lett. 410 (2-3), 485-489 (1997)			
3 (sites)			
Motoyama,J., Takabatake,T., Takeshima,K. and Hui,C.-C.			
patch2, a second mouse patched gene is co-expressed with Sonic			
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Nature Genet. 18, 104-106 (1998)			
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 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Aldrich, E., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beld, F.,
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
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 JOURNAL Unpublished
 TITLE Homo sapiens chromosome 17, clone RP11-762K23
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 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beld, F.,
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
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Perfect score: 5288
Sequence: 1 GAATTCGGGACCGCAAG.....TATGAAGAAAGCCCGAATT 5288

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_36.*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT.*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT.*
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21: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
22: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5288	100.0	5288	17 T14220	Human patched gene
2	5288	100.0	5288	20 V64093	Human patched gene
3	5281.6	99.9	5288	19 V21590	Human patched gene
4	4684.8	88.6	6568	19 V15949	Human patched gene
5	3801.2	71.9	5187	19 V21587	Human patched gene
6	3801.2	71.9	5187	20 V64092	Human patched gene
7	3801.2	71.9	5187	20 V64099	Human patched gene
8	3798.4	71.8	5187	19 V21589	Human patched gene
9	3778	71.4	5187	17 T14218	Human patched gene
10	1176.4	22.2	4030	20 Z31717	Human patched-2 co
11	1173.2	22.2	4391	20 X89478	Human patched-2 co
12	1171.6	22.2	3453	21 A09081	Human patched-like

13	593.8	11.2	2082	20 Z31729	Human patched-2 co
14	472.2	8.9	1734	19 V15998	Human patched-2 co
15	433.8	8.2	2032	19 V69382	Human patched-2 co
16	427.2	8.1	445	20 V87142	Human patched-2 co
17	411.8	7.8	3900	16 V91660	Human patched-2 co
18	405	7.7	4434	20 V64100	Human patched-2 co
19	228	4.3	228	20 Z31719	Human patched-2 co
20	183.6	3.5	4004	20 Z31728	Human patched-2 co
21	137	2.6	12886	21 A09084	Human patched-2 co
22	132	2.5	228	20 Z31718	Human patched-2 co
23	85	1.6	114955	20 X53491	Human patched-2 co
24	77.8	1.5	114955	20 X53491	Human patched-2 co
25	77	1.5	345	17 T14224	Human patched-2 co
26	77	1.5	345	19 V21588	Human patched-2 co
27	77	1.5	345	20 V64101	Human patched-2 co
28	76.6	1.4	4550	20 X06873	Human patched-2 co
29	74.2	1.4	477	21 Z44307	Human patched-2 co
30	73.4	1.4	5029	20 X06874	Human patched-2 co
31	70.4	1.3	138	19 V69383	Human patched-2 co
32	69.2	1.3	1272	20 X09010	Human patched-2 co
33	69.2	1.3	4020	18 T91361	Human patched-2 co
34	69.2	1.3	4524	20 V33912	Human patched-2 co
35	68.4	1.3	126	21 A09082	Human patched-2 co
36	67.2	1.3	3946	18 T93610	Human patched-2 co
37	66.6	1.3	736	17 T14225	Human patched-2 co
38	66.6	1.3	736	19 V21586	Human patched-2 co
39	66.6	1.3	736	20 V64098	Human patched-2 co
40	65.6	1.2	1439	19 V64533	Human patched-2 co
41	65.6	1.2	1439	19 V44424	Human patched-2 co
42	65.6	1.2	1439	20 Z19334	Human patched-2 co
43	65.6	1.2	1439	20 Z19122	Human patched-2 co
44	65.6	1.2	1439	20 Z37543	Human patched-2 co
45	65.4	1.2	334	20 V89418	Human patched-2 co

ALIGNMENTS

RESULT 1	
T14220	
ID T14220 standard; cDNA; 5288 BP.	
XX AC T14220;	
XX AC T14220;	
DT 30-JUL-1996 (first entry)	
XX DE Human patched gene.	
XX KW Patched gene; ptc gene; embryo development; cellular regulation;	
KW signal transduction; ligand; antibody; hedgehog protein;	
KW gene therapy; ss.	
XX OS Homo sapiens.	
XX OS Homo sapiens.	
XX FT Key	Location/Qualifiers
FT CDS	384..1427
FT	/*tag= a
XX PN WO9611260-A1.	
XX PD 18-APR-1996.	
XX PF 06-OCT-1995;	95WO-US13233.
XX PR 07-OCT-1994;	94US-0319745.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.	
XX PI Goodrich LV, Johnson RL, Scott MP;	
XX DR WPI: 1996-209842/21.	
XX P-PSDB; R75375.	
XX	

PT DNA encoding patched protein other than Drosophila patched protein -
 PT used to produce antibodies which detect or inhibit patched protein
 PT ligand signal transduction in cells

Example: Page 53-56; 70pp; English.

CC A cDNA clone (T14220) coding for the human patched protein (PTC)
 CC (R75375) was obtd. by screening a human lung cDNA library with a
 CC 1 kb portion of the mouse Ptc gene (see also T14218) and examination
 CC of isolated clones. The human Ptc gene has about 89% identity to
 CC the mouse Ptc gene. The 5' and 3' untranslated sequences are highly
 CC similar to mouse Ptc, suggesting conservation of regulatory
 CC sequences. The human Ptc gene can be used for prodn. of large
 CC amounts of recombinant PTC, as a probe e.g. to detect gene
 CC mutations, in gene therapy, to study embryo development, to produce
 CC transgenic animal models, etc.

CC Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 other;

Query Match 100.0%; Score 5288; DB 17; Length 5288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGGACCGCAAGAGTCCCGGGAAGCGCCCGAAGACAGAGCTCCTCGGCGC 60
 Db 1 gaattccgggggacccgaagagtgccgcggaagcgcccggaagacaggtccgctcgcgc 60
 QY 61 GCGGCGCTCTCGCTTCCCGCAACTGATGTGGGACAGCGCGCGCGGAGACCTCGGGA 120
 Db 61 gcggcgctcgcctcctccgcgaacttgatgtggcagcgcgcgcgagagactctcgga 120
 QY 121 CCCCCCGCAATGTGGCAATGGAAGCGCAGAGGTCTGACTCCCGGCGAGCGCGCGGCC 180
 Db 121 cccccgcgaatgtggcaatggaaagcgaggtctgactccccgcgagcgcgcgcc 180
 QY 181 GCAGGCGGCGAGCGCGCGCGCGGTGAGCAGCAGCGCGCGGTCTGTCTTAACCGAGGCC 240
 Db 181 gcagcgcgagcagcgcgcgcgctgtgagcagcagcgcgctgtctgttaaccgagcc 240
 QY 241 CGAGCGCGAGCAGCCTGCGCGCGAGCAGCGCTCTCGCAGCGCAGCGCGCGCGCGCAG 300
 Db 241 cgagcgcgagcagcctgcgcgcgagcgctcctcgcaagcgcgagcgcccgcgcgag 300
 QY 301 CAGCGCGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 Db 301 gacgcccagcagcgcgcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 360
 QY 361 GCGGCGGCGGCGCGCGCGCGCAATGGCTCGGTGTAACGCGCGCGAGCGCGCGAGACC 420
 Db 361 gcggcgcgcgcgcgcgcgcaacaatgctcggtgtgtaacgcgcgcgagccccagagcc 420
 QY 421 GCGGCGGCGCGCGCGCGCGCTGATCGGTGCCCGGAGCGCGCGCTGAGCGCGGAGGC 480
 Db 421 gcggcgcgcgcgcgcgcgctgtatcggtgcccgagcgcgcgcgctgagcgcgagagc 480
 QY 481 GCAGACGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 Db 481 gcagcgagcagcgggggtgcgcgctgctgcgcgcgcgagcgagactatctcacgcgc 540
 QY 541 CCAGCTACTGGAGCGCGCGCTCGCTGAGCAGATTCCAAAGGGAGGGCTACTGCGCC 600
 Db 541 ccagctactgagcgcgcgctcgtctgtgagcagattccaaagggaaggtactactgccc 600
 QY 601 GGAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTTATTAACCTGGTGTGTT 660
 Db 601 ggaagcgccactgtggtgagagcgaagtttcagagacttatttaacctgggtgtgtt 660
 QY 661 ACATTCAAAAAAAGTGGCGCAAGTTCTGTTGTGGGCTCTCATATTTGGGCGCTTGG 720
 Db 661 acattcaaaaaaagtgcgcaagttctgtgtgtggcctctcatatttgggctctgtg 720
 QY 721 CGGTGGGATTAAAGCAGCAACTCGAGACCAACGTGAGGAGCTGTGGGTGGAAGTTG 780

Db 721 cgttgagattaaagcagcaactcgagaccacgttggagagctgtggtgaggttg 780
 QY 781 GAGGACGAGTACGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 Db 781 gaggaagcagtaagtcgtgtaataataataataataataataataataataataata 840
 QY 841 TTAATCTCACTCATGTATACAGACCCCTAAAGAAAGAGGTGCTAATGCTCAACACAG 900
 Db 841 ttaatctcaactcatgtatcacgacccctaaagaagaaggtgctaatgctcaacacag 900
 QY 901 AAGCGCTCTTACACACCTGAGCTGGCAGCTCCAGGCGAGCGGTGTCTATATACATGT 960
 Db 901 aagcgctcttacaacacttgagctgcgacatccagccagcgctgtcctatatactgt 960
 QY 961 ACAACAGCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
 Db 961 acaacagcagtgaaatltggaacatltgtltacaataatacaagagagctatacaga 1020
 QY 1021 CAGGTTACATGATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
 Db 1021 caggttatactgatacagataataataataataataataataataataataataata 1080
 QY 1081 ACTGCTTGGGAGAGGCGGAAATTAAGTCTGGAGACAGCATACCTCTAGTTAAACCTC 1140
 Db 1081 actgcttgggagagggcgaaattacagctcggagacagcatacctcctagttaaac 1140
 QY 1141 CTTTGGCGTGGCAACCTTCCGAGCTTGGATTCCTGGAAGAGTTAAAGAAATTAATTA 1200
 Db 1141 ctttggcggtggaacacttgcaccccttggaaatcccttggaaagagttaaagaaat 1200
 QY 1201 ATCAAGTGGACAGCTGGAGAGGAATGCTGAATTAAGCTGAGGTTGCTATGATCATG 1260
 Db 1201 atcaagtggacagctggagaggaatgctgaattaaagctgaggttgcatactgata 1260
 QY 1261 ACCGCGCTTGGCTCAATCCGCGCGATCCAGACTGCGCGCGCACAGCGCGCGCAACAA 1320
 Db 1261 accgcccccttgcataatccgcgcgaatccagatgccccgcacagcccccaaaaa 1320
 QY 1321 CAACCAAACTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 Db 1321 caaccaaaactcttgatgatatgccccctgttggaaatggtgatactgatactcaaga 1380
 QY 1381 AGTATATGACTGGCAGAGAGAGATTAATGATGATGATGATGATGATGATGATGATG 1440
 Db 1381 agtatatgactggcagagagagatgattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
 QY 1441 AACTGCTAGCGGCCATGCTGCGAGACCATGTTCCAGTTAATGACTCCCAAGCAATGT 1500
 Db 1441 aactgctagcgcccatgctgcgagacatgltccagttaatactcccaagcaatgt 1500
 QY 1501 ACGAGCACTTCAAGGGGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Db 1501 acgagcacttcaagggtatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
 QY 1561 CAGGCATCTTGAGAGCGCTGAGAGAGACATATGTTGAGAGGTGTTATCAGATGTCGAC 1620
 Db 1561 caggcattcttgagagcgctgagagagacatattgttgagaggtgattcaagagtg 1620
 QY 1621 AGAAGCTCAGCTCAAAAGGTGCTTCTTCCACACACACACACCTTGAGAGCATCTGA 1680
 Db 1621 agaagctcagctcaaaaggtgcttcttccacacacacacacacacacacacacac 1680
 QY 1681 CTTTCTGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 Db 1681 ctttctgagagtgatgagtgatgagtgatgagtgatgagtgatgagtgatgagtgat 1740
 QY 1741 CTTGCTTAACCATGCTGCTGAGAGTGTCTCAAGTCTCAAGTGTCTGAGAGTGTCTG 1800
 Db 1741 cttgcttaaccatgctgctgagagtgctcaagtctcaagtgtcagtgagtgagtgag 1800
 QY 1801 GCGTCTGCTGTTGCACTGTCACTGCTGAGAGACTGAGGCTGTGCTATGATGAGGAA 1860

Db 1801 gggctcgtcgtgtgtcagctcagtgctgcaagactggtcgtgtcattatgctcgaa 1860
Qy 1861 TTTTCCTTTAAAGCTGCAACAACATCAGGTTTTTCCATTTCTGCTCTTGTTGGTGTGG 1920
Db 1861 ttctcttaacgctgtcacacaactcaggttttgcattcttcgctctgtgtgtgtgtg 1920
Qy 1921 ATGATGTTTTTTCTTTCTGCCCCACGCCCTTCAATGTAAGACAGACAGATAATAATCCCTT 1980
Db 1921 atgatttcttctctctgtcccaacgctctcagtgaaacagagacagataaaagatccctt 1980
Qy 1981 TTGAGACACAGACCGGAGGATGCTCTGAAGCCACAGAGACAGCCAGCTGGCCCTCACGTCCA 2040
Db 1981 ttgagagacagagaccggtggaatgtcctgtaagcacaagagccaggtgtgcctccacgtcca 2040
Qy 2041 TCAGCAATGTACAGACCTTCTTCATGGCCGCGTTAATCCCAATTCCTGCTGCGGGCGT 2100
Db 2041 tcagcaatgtcacagacctctctcattgagcgcgttaatcccaattccgctctcgtcggt 2100
Qy 2101 TCTCCCTCCAGGACGCGGTAGTAGTGGTTTCATTTTGGCATGGTTCTGCTCATTTTTC 2160
Db 2101 tctccctccagcagcgtgtagtggttgcatttctgcatggttctgtcctcatttctc 2160
Qy 2161 CTGCAATTTCTCAGCATGGATTTATATGACGCGAGAGACAGAGACGATGATTTTCTGCT 2220
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Qy 2221 GTTTTACAAGCCCTCGCGTACAGAGAGTAGATTGAGTTGAACCTTCAGGCCCTACCCGACA 2280
Db 2221 gtttacaagccctcgtcgtcagagagtgattcaagttgaaacctcagcctcacacggaca 2280
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Qy 2341 AAACGAGATTACCATGCTCAGTCCAGTCTCCAGTCCGACAGAGTAGACAGCCCCACACGC 2400
Db 2341 aaacgagattacacatgagatctcagcttccagcctccgacagagatgaaccccccaacgc 2400
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Db 2521 cccagctctcagactccagctccactgctcgcgtccgagccccctgttcgaagtgtgacactct 2580
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Db 2581 catcttctgtgagaaacatactgtctctctctcttgaacccaagaagcgaagtgtg 2640
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Db 2701 acggcgctgacacttacgagacatgtactcctgggaaacacagagataatgacttattgtcgt 2760
Qy 2761 CACCAATTCAAATCTTTTCTTCTACACATGTATATAGTACCCAGAAAGCAGACTACC 2820
Db 2761 cacaattccaataactcttctcttcaacaatgtatatagtaaccagaagaagactacc 2820
Qy 2821 CGAATTCAGACGACTTACTTAGACCTACACAGAGTTTCAAGTATAGTGAAGTATGTGA 2880
Db 2821 cgaattccagacacttaacttaacgaactacaagagattcagtaacgttgaagtatgtta 2880
Qy 2881 TGTGTGAGAAAAAACAACAGCTTCCAAAAATGTGGCTGACACTTACAGACTGGCTTC 2940
Db 2881 tgttgtgaagaataaacaagcttcccaaatgtgctgcaactacttcaagagactgtgcttc 2940

Qy 2941 AGGACCTTCAAGATGCATTTTGACAGTAGCTGGGAAACCGGAAATATCATGCCAAACATTT 3000
Db 2941 aggacattcagatgcatcttgacagtgactggtgaaacccggaaatcatatgcacaacattc 3000
Qy 3001 ACAAGAATGATTCABACGATGAGATGCTTGGCTACTCAAAATCCTGTGTGCAAAACCGCACCC 3060
Db 3001 acaagaatgatatcagacgatgtgactcctgtcttacaacactcctgtgtgcaaacaggcagcc 3060
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Db 3061 gcgataagcccatgcacatcagccagttgtactcaaaacagctcgtgtggaatcgagatgca 3120
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Qy 3181 CGTATGCTGCTCCACAGGCCAATCCGGCCACACCCAGACCAATGGGTCCACGACAAAG 3240
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Db 3241 ccgactacatgctgtgaaacaaggtcgtgaaatcccgacagagcccatcgaatgagatgc 3300
Qy 3301 AGTTCCCTTTTCTACCTCAACGGGTTGCGGGACACCTCAAGACTTGTGAGAGCAATTGAAA 3360
Db 3301 agttcccttctactcaacaggtgtgtcggtgaaaccccaagacttgtgtgagagcaattgaaa 3360
Qy 3361 AAGTAAGACCATCTGACAGCAACATATACGAGCTTGCGGTCTGTCAGTTACCCCAACGCGT 3420
Db 3361 aagtaagacatctctgcagcaactatacagccttgggtcgttccagttaccccaagcgtc 3420
Qy 3421 ACCCTTCTCTCTTGGGAGAGTACATGGGCTCCGCACTGGCTGCTGCTGTATCA 3480
Db 3421 acccttctctctctcgtggagacgtataatccgcgtcccgcaactgtgcgtgtgttca 3480
Qy 3481 GCGTGTGTGGCTGACATTCCTGCTGTGCGCTGCTCTTCTGAAACCCCTGTGACGG 3540
Db 3481 gcgtgtgtgtgcctgcacatctcctgtgtgcgtgtcttctctcctgcgaacccctgtgcg 3540
Qy 3541 CCGGGATATATGTGATGTGCTCTGCGGCTGATACAGCTTCGAGCTTGGCATATGAGGCC 3600
Db 3541 ccgggataatattgtatgttgccttgcgtgctgatacagcttcgagcttgcagatgata 3600
Qy 3601 TCATCGGAATCAAGCTCAAGTGGCGGCTGCGCTGCTGATCTGATCGCTTCTGTTGGCATG 3660
Db 3601 tcacggaatacaagctcagctgtgcgtgtgcgtgtgttccatcagcttctgtgtgacatg 3660
Qy 3661 GAGTGAAGTTCAACGTTGACGTTGCTTGGCTTCTGACGGCCATCGGCGACAGAACMC 3720
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Db 3721 gcagggctgtgtgtccttgcgtgagcaaatgttgcacccgttccgtgatagtgcgctgtcca 3780
Qy 3781 CTTGCTGAGGAGTGTGATGCTGCGGGGATCTGAGTTCGACTTCATTTGATGAGATTTCT 3840
Db 3781 ctctgctgagaggtgtcgtatgtctgtgcggagatctgagttcgaactcatctgtlcaagttatctc 3840
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 QY 4081 GCGTCAGAGAGAGCTTGGGCACTACGAGGCCAGAGGGCGGGAGCCCTGCCACC 4140
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 QY 4141 AAGTATGTGGAAAGCCAGAAAACCCGCTTCGCCACATCGTGGTCCATCCG 4200
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 Db 4141 aagtgatctgtagagccacagaaaacccgctctcgccactccactctggtccatcccg 4200
 QY 4201 AATCCAGGCATACCCACCTTCGAACCCGAGACAGCCGCCACCTGGACTCGGTC 4260
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 QY 4261 TGCTCCCGGAGCGCAAGGCCAGAGCCCGGAGGAGCCCGCCAGAGAAAGTTGTGGC 4320
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 Db 4261 tgcctccggaagcaggaagccagcccgacagggacccccccagagaggtctgtggc 4320
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 QY 4381 CTAGCAATAGGCGCCGCTGGGGCCCTCGCGGGGCCGTTCTGACAACCTCGGAACCCAG 4440
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 Db 4381 ctagaacaatagggccgcgtggggccctcgggggccgctctcacaacccctcgaaacccag 4440
 QY 4441 GGTCCACTGCGCATGGGAGAGCTCCGCGCGGCTACTGCGCAGCCCATCACACTGTACGG 4500
 |||||
 Db 4441 ggtccactgcatgggagagctccgcgccgctacgctacgacagccacacacacgtgacgg 4500
 QY 4501 CTTTGCCCTCCGTGACTGCTGCGCTGACCCCGCGCTTCCTCGGCGCTGGGCGGAGACC 4560
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 Db 4501 ctctgcctccgtgactgctgacgctgacccgcgcgtctccctggcctggcggaacc 4560
 QY 4561 CCCGAGGGGAGACTCTGCCAGGCTACCTGAGACTGACACGCGCTGTTTGAGAGACCCC 4620
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 Db 4561 cccgaggggagactctgcccaggtacacctgagacacagcgcgtcttgagagaccccc 4620
 QY 4621 ACGTGCCCTTCGACGTCGCGGTGTGAGAGAGGATTCGAGAGTGGAGATGATGACTGC 4680
 |||||
 Db 4621 acgtgcccctccacgctccggtgtagagagagatcgaaaggtggaagtcattgagactgc 4680
 QY 4681 AGGAGTGGAAATGCGAGAGAGAGGCCCGGGGAGAGAGCTCAACTAGAGGTGATTAAT 4740
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 Db 4681 aggacgtggaatgtagagagagagcccgaggagacagctccaaactgagaggtgataaat 4740
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 Db 4741 ctgaagcaaaagagcacaagatltgaaacccccccacactctctccagagactgctt 4800
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 QY 4861 ACTGTAAACGATTTGATTTTGTGTAATATTTCTATAATATTTAAAGATGTGACACA 4920
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Db 5101 ttacttgataaatctctagcaaatatgtcttatgtataagatattttgtgaaggttc 5160
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 Db 5161 tgtttaaataattttaaatattgtacatacaacccctgtgtagtagtaagaattctactgtt 5220
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 Db 5221 aacttcaaacacagctatgtgtataatttttgtttaatgagcagatatagaaagagc 5280
 QY 5281 CCGGAATT 5288
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 Db 5281 ccggaatt 5288
 RESULT 2
 V64093
 ID V64093 standard; cDNA; 5288 BP.
 XX
 AC V64093;
 XX
 DT 26-JAN-1999 (first entry)
 XX
 DE Human patched gene.
 XX
 KW Human: patched gene; diagnosis; treatment; developmental disorder;
 KW cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
 KW sperm production; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 384..4727
 FT CDS /*tag= a
 XX
 PN US5837538-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 06-OCT-1995; 9505-0540406.
 XX
 PR 06-OCT-1995; 9505-0540406.
 PR 07-OCT-1994; 9405-0319745.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Goodrich LV, Johnson RL, Scott MP;
 DR WPI; 1999-023461/02.
 DR P-PDB; W72969.
 XX
 PT Nucleic acid encoding vertebrate patched protein and related
 PT transformants - used to express poly:peptide(s), useful for
 PT diagnosis and treatment of developmental disorders or cancer, and in
 PT healing of injured tissue
 XX
 PS Claim 1: Column 59-64; 38pp; English.
 CC
 CC The present sequence represents the human patched (ptc) gene. Cells
 CC containing and expressing the ptc gene are used for the recombinant
 CC production of the protein. These in turn are useful: (1) for generating
 CC antibodies (Ab); and (1i) to screen for specific-binding ligands
 CC (potential therapeutic agonists and antagonists). The ptc gene, or its
 CC fragments, are used to isolate related sequences from other mammals; to
 CC identify mutations (particularly those associated with genetic diseases
 CC such as spina bifida and other developmental disorders); to monitor
 CC expression levels in tests (to determine relationship with sperm
 CC production) and to isolate 5'-non-coding sequences (used to study
 CC embryonic development and to provide regulated expression of proteins).
 CC The complete gene can be used in gene therapy, including expression of
 CC antisense molecules, and to generate transgenic animals for studies of
 CC embryonic development. Ab are used diagnostically to determine the

CC p1c protein on cell surfaces and as competitive inhibitors of signal
 CC transduction through the p1c ligand. Cells that have been engineered to
 CC express the p1c protein can be used to promote regrowth and healing of
 CC damaged tissue (e.g. growth of new teeth) and regulation of the p1c
 CC protein expression may be useful in cancer treatment (it may control the
 CC Mnt-1 oncogene).

XX Sequence 5288 BP: 1182 A; 1530 C; 1417 G; 1159 T; 0 other;

Query Match 100.0%; Score 5288; DB 20; Length 5288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 gccggctctgctcttccgccaactgagatggtgagcagcgcgccgagagacctcgga 120
 QY 121 CCCCCGCGCAATGTGGCAATGGAAGCGCAGAGTCTGACTCCCGGACGCGCGCGGC 180
 Db 121 cccccgccaatgtggcaatggaaagcgcaaggtctgactcccgcaagcgccgagcc 180
 QY 181 GCACGCGCAGACGCGCCCGCGCTGTGACGACGACGACGCGCGCTGTGTCAACCGAGCC 240
 Db 181 gcaagcgagcagcgccgctgtgacgacgacgagcgctgtgtctgtcaacgagagcc 240
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 Db 241 cgagcccgagagctgtggcgagagctctgcaagccgagggcgccagcgccagcgcc 300
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Db 5221 aacttcaaacacagctatgctatgataatttlttltlaatgagcaqatatagaagaagc 5280

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QY 5281 CCGGAATT 5288
Db 5281 ccggaatt 5288

RESULT 3
V21590
ID V21590 standard; DNA; 5288 BP.
XX
AC V21590;
XX
DT 25-JUN-1998 (first entry)
XX
DE Human patched (ptc) protein encoding cDNA.
XX
KW Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
KW wound healing; ageing; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 384..4727
FT /tag= "a
FT /product= "Human patched protein"
XX
PN W09745541-A2.
XX
PD 04-DEC-1997.
XX
PF 02-JUN-1997; 97MO-US09553.
XX
PR 31-MAY-1996; 96US-0656055.
XX
PA (RECC ) UNIV CALIFORNIA.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Epstein E, Goodrich LV, Johnson RL, Oro A, Scott MP;
XX
DR WPI; 1998-032648/03.
XX
DR P-PSDB; W52200.
XX
PT Patched protein other than Drosophila melanogaster patched protein -
PS used for characterizing the phenotype of a tumour
XX
PS Claim 4; Pages 73-76; 86pp; English.
XX
CC This genomic DNA encodes a human patched (ptc) protein. This can be used
CC to construct an expression cassette comprising an altered patch or
CC hedgehog gene. The expression cassette comprises a nucleic acid encoding
CC a patched protein other than a Drosophila melanogaster patched protein,
CC or fragment of at least 12 nucleotides in length, as other than an intact
CC chromosome under transcriptional control of a transcriptional initiation
CC region, and a transcriptional termination region, both functional in an
CC expression host. A genetically engineered mammalian cell comprising this
CC expression cassette as an extrachromosomal element or integrated into the
CC genome of the cell can be predisposed to develop basal cell carcinoma as
CC a result of the transfection. By analysing DNA, functional analysis of
CC patched protein function, or by detecting antibody binding to abnormal
CC patched protein, a genetic predisposition to developmental abnormalities
CC and cancer can be diagnosed. This analysis can also be used for
CC characterizing the phenotype of a tumour, particularly a carcinoma,
CC especially a basal cell carcinoma. The methods can also be used for
CC characterising transitional cell carcinoma of the bladder, meningiomas
CC medulloblastomas, etc. The modified cells comprising the expression
CC cassette can be used to determine the role of different exons of the
CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal
CC models created from these cells can be used as animal models for
CC carcinomas of the skin. The patched protein of mosquito, butterfly or mouse
CC beetle or alternatively, a mammalian patched protein of human or mouse
CC can be used to identify ligands or substrates that bind to, modulate, or
CC mimic the action of patched gene. These agents could be used as tumour
CC suppressors, cell adhesion promoters (e.g. In wound healing and ageing).

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Db 2041 tcagcaatgtcacaagcccttctcatgtgcgcgttaatcccaattccgcctctcgcgcgt 2100
QY 2101 TCTCCCTCCAGGACGCGTAGTAGTGATGATTCATTAATTTTGCCATGATTTGCTCATTTTC 2160
Db 2101 tctccctccagagcgagtagtagtgcgttcaatttgcatttgcatttcttcc 2160
QY 2161 CTGCAATTTTCAGATGGATTTATATGACGCGAGAGACAGAGACTTGATATTTTCTGCT 2220
Db 2161 ctgcgaattctcagatgattatataatcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2220
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Db 2941 aggaacttcagatgtcatttgcagtgacttgcggaacccgcgcgcgcgcgcgcgcgcgcgc 3000
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OY 5281 CCGGAATTT 5288
DB 5281 CCGGAATTT 5288

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RESULT 4
ID V15949 standard; cDNA; 6568 BP.
XX
AC V15949;
XX
DT 27-MAY-1998 (first entry)
XX
DE Nevoid basal cell carcinoma syndrome (NBCCS)(PTC) protein encoding cDNA.
XX
KW Nevoid basal cell carcinoma syndrome; NBCCS; PTC; PATCHED; detection;
XX Tumour suppressor; human; mutation; Gorlin's syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..441
FT CDS 442..4332
FT 3'UTR 4333
FT /tag= b
FT /product= "NBCCS (PTC) protein"
FT /tag= C
XX
PN WO9743414-A2.
XX
PD 20-NOV-1997.
XX
PE 16-MAY-1997; 97WO-US08433.
XX
PR 16-MAY-1997; 97US-0017906.
PR 17-MAY-1996; 96US-0017906.
PR 21-MAY-1996; 96AU-0000011.
PR 07-JUN-1996; 96AU-0000363.
PR 14-JUN-1996; 96US-0019765.
XX
PA (USSH ) US SEC DEPT HEALTH.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gerrard B, Gillies S, Goldstein A, Dean MF, Gallani MR;
PI Lefell DJ, Negus K, Pressman C, Shanley S, Smyth I;
PI Unden AB, Vorechovsky I, Wainwright B, Wickling C;
PI Zaphiropoulos PG, Chevenix-trench, Tofgard R.
XX
WP1: 1998-008883/01.
P-PSDB: W47157.
XX
PT Nevoid basal cell carcinoma syndrome tumour suppressor gene - useful
PT for detection of pre:disposition to basal cell carcinoma(s)
XX
PS Claim 1; Fig 8; 148pp; English.
XX
CC This cDNA encodes a nevoid basal cell carcinoma syndrome (NBCCS)
CC (PTC) protein. This nucleic acid specifically hybridises, under stringent
CC conditions, to a second nucleic acid consisting of a 6568 (full-length
CC sequence), 1732 (exon 1a, b) (V15998) or 659 (exon 2a) (V15999) base pair
CC sequence, in the presence of a human genomic library. The PTC polypeptide
CC when presented as an antigen elicits the production of an antibody which
CC specifically binds to a polypeptide encoded by the above three sequences.
CC The NBCCS gene and its protein product, is a tumour suppressor, and is a
CC homologue of the Drosophila PATCHED (PTC) gene. Detection of the NBCCS
CC nucleic acid, in particular abnormal sequences, by hybridisation assays
CC is useful for detecting a predisposition to NBCCS or to a basal cell
CC carcinoma (also known as Gorlin syndrome). Alternatively, detection is of
CC the polypeptide and is carried out by immunoassay. Vectors comprising
CC this nucleic acid can be used to treat NBCCS. The PTC polypeptide can
CC mitigate symptoms of NBCCS in an organism. The NBCCS nucleic acid
CC includes one or more mutations, chosen from Exon-5 693insC, Exon-17
CC 2988del18bp, Exon-21 3538delG, Exon-22 64302T, Exon-12 1711insC, Exon-12
CC 1639insA, Exon-16 2707delC, and intron-17 3157-2A to G. The mutation may
CC be a nonsense or frameshift mutation. Frameshift mutations are chosen
CC from 244delC, 27insA, 464insAC, 693insC, 804del137, 877delG, 929delC,

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CC 1370del176, 1393insTGGC, 1444del16, 1497dup8, 1639insA, 1711insC,
CC 2183delATC, 2320insAA, 2392delA, 2574delA, 2585delC, 2596complex,
CC 2707delC, 2749insC, 2749dup7, 2988del18bp, 3014insA, 3352delAT and
CC 3538delG. The mutation may be missense, chosen from G391T, G1148A,
CC G1568A, G1525T, C2050T, C3015A, G3193C AND G4302T. Alternatively,
CC the mutation alters mRNA splicing and is chosen from A1055-2C, 3157-2A to
CC G and 1493-8ins21. All these mutations are claimed but their sequences
CC are not provided in the specification.

XX Sequence 6568 BP; 1499 A; 1780 C; 1676 G; 1610 T; 3 other;

Query Match 88.6%; Score 4684.8; DB 19; Length 6568;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 4692; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 585 GGAAGAGCTACTGCGCGGAAGCGCCACTGTCGTGAGAGGAGATTTCAGAGCTTTA 644
DB 190 gggaaagctactgagccggaaagcgcgctgctgctgagagagagttccagagactctta 249
QY 645 TTTTAACTGGGTTGTTACATTTCAAAAAAACTGCGCAAGTTCTTGTTGGGCTTCCTC 704
DB 250 tttaactggtgttaccattcaaaaaaactgcgcgaagttcttggttggtggtcctc 309
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QY 765 CTGTGGGTGGAAGTTGGAGAGAGAGTAAAGTGAATTAATTAATTAATTAATTAATTA 824
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DB 490 aatgctccgagcagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 549
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DB 610 gagctatcacagaacaagttacatgatacagatacagatacagatacagatacagatac 669
QY 1065 ATTATTAACCTTTGGACCTCTCTGGAGAGGCGCAAAATTACAGTCTGGACAGCATAC 1124
DB 670 attattacaccttgagctgcttctggaagggcgaattacagctcgggagcagcatac 729
QY 1125 CTCTAGTAAACCTCTCTGCGTGGAGCAAACTTGACCTTTGGAATTCCTGGAAGAG 1184
DB 730 ctccctagataaactcctcttggtggtggtggtggtggtggtggtggtggtggtggt 789
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DB 1870 cagggcttacaacgacacacacagcaataaccgctacagacccccccactccctcagcag 1929
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QY 2505 ACAAGGACCTGCTCTCCCATTTCTCGAATCTCAGCTTCAGCTTCAGCTTCAGCTTCAG 2564

Db 2110 acaaggaaactgctctcccaagctctccgaactcccaactccctcagcctcagccccctgt 2169
QY 2565 ACGAAGTGGACACTCTCATCTTTTGGCTGAGAAGCACTATGCTCTTCTCTTGAACCA 2624
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Db 2230 aaagccaagtagtggtagctctctctctctctgagcttgagg999tcaagcctttagc 2289
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Db 2290 accaccgagtgagagagagggctggaactcagacatgtaccccggaacccagagaa 2349
QY 2745 TATGACTTATTTGCTGCAATTTCAATACTTTTCTTCTACAGATGATATAGTACAC 2804
Db 2350 tatgacttatctgctgacaaactcaactcttctctctcaaaaatgatatagtcacc 2409
QY 2805 CAGAAGCAGACTACCCGAATATCCAGACATTTACTTTACGACCTTACACAGAGTTTCAGT 2864
Db 2410 cagaagaagactaccgcaataccagcaacttaacttaagcaactcaacagagattcagt 2469
QY 2865 AACGTGAAGTATGTCATTTGGAAGAAAACAAGAGCTTCCCAATGTGGCTGCCTAC 2924
Db 2470 aagctgaagtagtcaatgtctggaagaaaacaacagctcccaaaatgtgagctac 2529
QY 2925 TTCAAGACTGGCTTCAGAGGACTTCAGAGATGATTTGACAGTGGGAAACCGGAA 2984
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QY 4665 GAAGTATGAGTGTGAGGAGCGAGTGGAGATGGAGAGAGGCGCGGGGAAGCATGCTCACAC 4724
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QY 4725 TGAAGGTGATTAATGTAAGCAAGCAAGCAAGATTCGAAACCCACCACCT 4784
 DB 4330 tgaagggtgataaattcgaagcaagagcaagattggaacccccaccacct 4389
 QY 4785 CTTTCCAGAACTGTTGAGAGCACTGTTGAGTATGAAAGATGCCCTGTCAGG 4844
 DB 4390 ctctcagaactcgtgaagagagactcgtgagatcagaaagaatgccctgtcgaag 4449
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 DB 4450 aacgaagctatcgttactcgttaaccgattgtatatttctgtaaatatttcataat 4509
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 DB 4510 ttaagagatgatacaatglttaataatagaagaaagatgtaaaatgltatgaltgagc 4569
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 DB 4690 ttaaatattgtataatttactgtataattcattgcaaatattgcttataatagatt 4749
 QY 5145 ATTTGTAAGGTTTCTGTTAAATATTTTAAATTTGCATATCAACCCGTGTGTACT 5204
 DB 4750 attctgaagagcttcgtttaaataattttaaattgcatatcaacccgtgtgtagt 4809
 QY 5205 ATGAAATGTTACTGTTAACTTTCAACAGCGTATGCGTATATTTTGTTAATGAG 5264
 DB 4810 atgaaatgttactcgttaactttcaacacagctatgcgtgataatttttgtttaaag 4869
 QY 5265 CAGATATGAAAGAACCCCGAATT 5288
 DB 4870 cagatatgaagaaagcagctaat 4893
 RESULT 5
 V21587 standard; DNA; 5187 BP.
 AC V21587:
 XX 25-JUN-1998 (first entry)
 DE Precis coenia (butterfly) patched (ptc) protein encoding DNA.
 XX Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
 KW wound healing; ageing; Precis coenia; butterfly; ss.
 OS Precis coenia.
 XX W09745541-A2.
 PN W09745541-A2.
 PD 04-DEC-1997.
 PF 02-JUN-1997; 97WO-US09553.
 PR 31-MAY-1996; 96US-0656055.
 PA (REGC) UNIV CALIFORNIA.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Epstein E, Goodrich LV, Johnson RL, Oro A, Scott MP;
 DR WPI, 1998-032648/03.
 PT Patched protein other than Drosophila melanogaster patched protein -
 used for characterising the phenotype of a tumour

XX Claim 2; Pages 49-51; 86pp; English.
 PS
 XX This DNA is stated to encode a *Precis coenia* patched (*ptc*) protein and
 CC is identical to the mouse *ptc* cDNA. This can be used to construct an
 CC expression cassette comprising an altered patch or hedgehog gene. The
 CC expression cassette comprises a nucleic acid encoding a patched protein
 CC other than a *Drosophila melanogaster* patched protein, or fragment of at
 CC least 12 nucleotides in length, as other than an intact chromosome under
 CC transcriptional control of a transcriptional initiation region, and a
 CC transcriptional termination region, both functional in an expression
 CC host. A genetically engineered mammalian cell comprising this expression
 CC cassette as an extrachromosomal element or integrated into the genome of
 CC the cell can be predisposed to develop basal cell carcinoma as a result
 CC of the transfection. By analysing DNA, functional analysis of patched
 CC protein function, or by detecting antibody binding to abnormal patched
 CC protein, a genetic predisposition to developmental abnormalities and
 CC cancer can be diagnosed. This analysis can also be used for
 CC characterising the phenotype of a tumour, particularly a carcinoma,
 CC especially a basal cell carcinoma. The methods can also be used for
 CC characterising transitional cell carcinoma of the bladder, meningiomas
 CC multiblastomas, etc. The modified cells comprising the expression
 CC cassette can be used to determine the role of different exons of the
 CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal
 CC models created from these cells can be used as animal models for
 CC carcinomas of the skin. The patched protein of mosquito, butterfly or
 CC beetle or alternatively, a mammalian patched protein of human or mouse
 CC can be used to identify ligands or substrates that bind to, modulate, or
 CC mimic the action of patched gene. These agents could be used as tumour
 CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing).
 XX
 SQ Sequence 5187 BP; 1165 A; 1412 C; 1337 G; 1270 T; 3 other;

Query Match 71.9%; Score 3801.2; DB 19; Length 5187;
 Best Local Similarity 88.1%; Pred. No. 0;
 Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

QY 446 CGGTGCCCCGAGCGCGCTGAGAGCGGAGCGGAGCGGAGCGGCTGCGCG 505
 DB 120 cggggcccttggcagagccggcgcgagagcgcaagagccggggagccgcagc 179
 QY 506 TGTGCGCGCGCGAGCGGAGCTATCTGCACCGCCAGCTACTGCGACGCGCTTCGC 565
 DB 180 c---gcgcgcgcagcgcggaactatctgcacgcgcgcagctactgcgcgccttcgc 236
 QY 566 TCTGAGCAGATTTTCCAGAGGGAAGGCTACTGCGCGGAAAGCCCACTGTGCTGAGAC 625
 DB 237 tctgagcagatltccaaggggaaggtactcgcgcgaaagcgcgctgtgctgagagc 296
 QY 626 GAACTTTCAGAGACTCTATTTAACTGGTGTGTTACATTTCAAAAAAAGTGGCGCAAGTT 685
 DB 297 gaagtltcagagactcttattttaaactcgtgtgtatcattcaaaaagactcgtgcagagtc 356
 QY 686 CTTGGTGTGGGCTCTCATATTTTGGGGCTTCGGGCTGGATTAAGCAAGCAACT 745
 DB 357 ttgtgttgagggtctcccatatttggggccttcgtgtgagatlaagcagctaatc 416
 QY 746 CGAGACCAACGTGAGAGAGCTGTGGGTGGAAGTGGAGACGAGTAAAGTGAATTAAA 805
 DB 417 cgagaccaacgltgagagagctgtggtgagatltgltgagagtgagtgagtaaataaa 476
 QY 806 TTATACTGCGCAGAGATTTGAGAGAGGCTATGTTAATCTCAACTGATGATPACGAC 865
 DB 477 ttataccgctcagaagatagagagaggtatglttaattcccaactcatgataagac 536
 QY 866 CCTTAAAGAAAGGTGCTAATGTCTGACCAAGAGAGGCTCTCAACACCACTGCACTC 925
 DB 537 tccaagaagaagcgctaatgtctcgcacacagaggtctctcgtcaacaactgtgactc 596
 QY 926 GGCACCTCAGGCGCAGCGCTGTCCATGATATGATGTAACAGGCACTGGAATTGACACA 985
 DB 597 agcactccagcgctcgtgtgacgtctacatgataacagagcaatggaagtgtgagaca 656

QY	986	TTTTGCTTACAAATTCAGGAGAGCTTTATCACAGAAACAGGTTACATGATCATGATTAATAGA	1045
Db	657	tttggcttctaaatctcaggggaacttctacgagacaagttacatgattcaagataataga	716
QY	1046	ATATCTTTACCCCTGTTTATTAATTTTACACCTTTTGAGCTGTTCCGGAAGGGGGAATTT	1105
Db	717	atacctttaccccttgcttcaatacattacaccccttggacgtctcttggaaagggaagaagct	776
QY	1106	ACAGTCTGGAGACGATACCTCTCTAGTAAACCTCTTTGGGTGGAACAACTTGCACCC	1165
Db	777	acagtcggagacagcatctacccctcagtaagcctcctcttcaggttgcacaacttgcacc	836
QY	1166	TTTTGGAAATTCCTCGGAGAGCTTTAAAGAAATTAACCTTAACTGATGACAGCTGGAGAAAT	1225
Db	837	cttggaaattcccttagaagagttlaaagaaaaaataactcccaagtgagacgcctggagagaaat	896
QY	1226	GCTGATTAAGGCTGAGGTTTGTCATGTTTACATGAGACCGGCCCTGCTCAATCCGGCGGA	1285
Db	897	gctgtaataaagccgaagatctggcacttggtatcatcagtaagcgccttgccttaaccagccga	956
QY	1286	TTCAGACTCCCGCGCCACAGCCCCCAACAAAAATTACCAAAACCTTTGATATGACCTT	1345
Db	957	cccaagatgcctctggccacagccccccttaacaaaaatlaaccaaaccctcttatgtgacct	1016
QY	1346	TGTTTTGAAATGGTGAAATGTCATGCTTTATTCACAAAGTATATACACTGCGAGGAGGATT	1405
Db	1017	tgatttgaaatgtgtgagtgctcaaggttataccaggaagtatatgcatctggcaaggagaagtt	1076
QY	1406	GATTTGGCTGGCACAGTCAGAACAGCACACTGGAAAACTGTCACGCCCCATGCGCTGCA	1465
Db	1077	gatttggtgtgttaccgttaagaatgatccactggaaaaacttgtaagcgtcagccctgcga	1136
QY	1466	GACCATGTTCTCAGTTTAAATGATGCTCCCAAGCAAAATGTCAGACACTTCAAGGGTAAAGGTA	1525
Db	1137	aaccatgtctccagttatgaatccccaagcaaatggtatgaacacttccagggtcttaagctta	1196
QY	1526	TGTTCTACACATCACTGGAAGGAGACAAGGACAAAGCGGACCCATCTGGAGGCTTGCGCAG	1585
Db	1197	tgctctctacatcaacttgaatgaaaacacaggcagccgcctatccttgaagccttgcagag	1256
QY	1586	GACATATGGAGGAGTGCTTATCAGAGTGTGGCACAGAACTCCACATCAAAAGGTGCTTTC	1645
Db	1257	gactaagtgaggagggtgttcatcaaaaagtgtgcgcccaaaactccactcaaaaagggtctcc	1316
QY	1646	CTTCAACACACGACCCTGGAGACATCCTGGAATCCTTCTCTGACGCTCAGTGTATCCG	1705
Db	1317	cttcaacaacacagacccttggagacatacctcaaaaactcctctctgtatgttcaagtgtcatcg	1376
QY	1706	CCTGGCCACCGGCTACTTACTACTATGCTCGGCTATGGCTGTCTAACATGCTGGCGTGGGA	1765
Db	1377	agtgagccagccggtactactcgtatgtcttgacctatgaccttlaacatgtctgcttggga	1436
QY	1766	CTGTCTCAAGTCCCAAGGGTGCCGTGGGGGTGGCTGTGGCGTCCCTGATTTACATGTCAGT	1825
Db	1437	ctgtccccaagtcaccaggtggtgcggtgggtgtgctgtgcgtgcctctgttgtgttgcgtgtcagt	1496
QY	1826	GGCTCAGAGACTGGGCGCTGTGCTCATTTGATCGGAATTTCTTTAAACGCTGCAACAACCTCA	1885
Db	1497	ggctcagagatctgggcctctctgctctcttgaatcttcttlaatgcttcgcgaacactca	1556
QY	1886	GGTTTTGGCAATTTCTGCGCTTGGTTGGTTGGTGTGAGTGAATGTTTTCTTGTGGCCACGCG	1945
Db	1557	ggcttctgcgcttcttgctcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1616
QY	1946	CTTTCAGTGAACAGGACAGATTAAGAATCCCTTTTGAAGAGACAGACCGGGAGTGCCTT	2005
Db	1617	atccagtgaaaaagagacaagaataaaggagattccatttggagacaggaacttggagtgctt	1676
QY	2006	GAAGGCGACAGGAGCCAGGCTGGGCGCTCAACGTTCATCAGCAATGTCAAGACTCTTTTCAT	2065
Db	1677	caagtgccatcccgagccaaggtgtggccctctcaactctccatcaagaaatgtataccgctcttcat	1736

QY	2066	GGCCGCGTTAATCCCAATTCCCGCTCTCGCGGGGTTTCCCTCCAGGCAGCGGTAGTACT	21235
Db	1737	ggccgcatlgtatcccatcccatccctccgacgagcttccctcccaagctctgctggtggt	17966
QY	2126	GGGTTTCATATTTTGGCATGGTTGTGTGTCATTTTCCGTGCAATTCCTGACATTTGATTTATA	21895
Db	1797	ggtatccaatttgcctcatggtcttctgtcatttcttcgtcaattccacgatgattcata	18566
QY	2186	TGACGACGAGAGACAGAGATGGATATTTTCTGCTGTTTTCATAAGCCCTCGCTGACAG	2245
Db	1857	cagaagctgagagacaagaatltgatatatttctctgtcttcaagaagccctctgctcagag	1916
QY	2246	AGTGATTCAGGTTGAACCTTAGCCCTACACCCGACACACAGACAAATTCGCCCTACAGCCC	2305
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QY	2306	CCCACTCCCTACAGAGCCACAGCGTTTGGCCATGMAAGCCAAATTACCATGGACGTCCAC	2365
Db	1977	cccccccccatlaccagacagccacagctctcgcccaagaaaccatatactctgtacgtcac	2036
QY	2366	TGTCCACCTCCGACGAGAGTACACACCCCAACAGCAGATGTACTACACACACCGGTGAGCC	2425
Db	2037	cgtltaagctccgacagagatgtacccctacaagacagctgtlactacaaccaacgcgcagcc	2096
QY	2426	GGCGTCCGAGATCTGTGTGACGCCCTGCACCGTGTACACAGACACCCCTGACGTGCCAGC	2485
Db	2097	acgctctgagatctctgtacaagcctgtltaacgtltaaccccaagacaacctcaagctgtcaag	2156
QY	2486	CCCAAGACACCCAGCTCCACAAAGGAGCCGTCCCAATTCGCAATTCGCAATTCGCAATTCG	2545
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QY	2546	CTGCGTCGAGGCCCCCTGTACAGAAAGTGAGACACTCTATCTTTTGTGATGAGAAGACTATGC	2605
Db	2217	ctgacgtccgagccccctctgacccaagtgagacacctctctgtctgcagagagaaactatgc	2276
QY	2606	TGCTTTTCCTTTGAAACCAAAAGCCAAAGTATGTGTATCTTCTTTTCTGGGCTTGGCT	2665
Db	2277	tctcttctctcttgaacccaagaagtgltgtltaatccttcttcttcttctggtctgtct	2336
QY	2666	GGGGGTCAGCTTTATTTGAGCACACCCGAGTGAAGAGAGAGGGCTGGACCTTTCGGGCAATTTG	2725
Db	2337	ggggggacgaccttatactgagagcaccgagatgagagagagggctgagacctcaagacattgt	2396
QY	2726	ACCTCGGGAACACAGAGATATGACTTTATTTGGTGTGCAATTAATTAATCTTTCTTTCTA	2785
Db	2397	tcccgaggaaccagagataatgacttcaagctgtccagtlcaagtaacttctctctcta	2456
QY	2786	CACACATGTATATATGTCACCCAGAACGACACTACCCGAATATCCAGCACTTACTTTAAGCA	2845
Db	2457	caacatgtatatagttaccaccaagaagcagactlaccgaatalatccaagaactactltaaga	2516
QY	2846	CCTACACAGAGATTTTCAGTAACTGTAAGTATGTATCTTTTGGAGAAACAAACAGCTTCC	2905
Db	2517	ccctcaaaagagtlctcaagaatgtlgaagtatgtltactgtctgtgagagagacaagaacttcc	2576
QY	2906	CAAAATGTGGTCGACTACTTTCAGAACTGAGCTTTCAGAGACTTCAGAGATTCATTTGACAG	2965
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QY	2966	TGACTGGGAACCGGGAATACTATGCCAAACAATTCACAGATGATCAGACGATGAGAT	3025
Db	2637	tgactggaagaactgtgagagtactgcaccaacaattataaanaatgtgactcagatgaagggct	2696
QY	3026	CCTTGCGTTCACAACTCCTGTGTGAAACCGGCACGCCGATTAAGCCCATGCACATCAGCCA	3085
Db	2697	ccctgccttacaactctctgtgtgagactctgtgcagccgagacaagcccatctgaactltagca	2756
QY	3086	GTTTGACTTAACAGCGCTGTGTGATTCAGATGTGCATCATTAATTCACAGCGCTTTCTTCAT	3145
Db	2757	glttgactaaacagcgtctgtglaagcagatgtgacatataatccagagcgcttcttaacat	2816
QY	3146	CTACCTGACGCGTGTGGGTAGCAACACCCCTCGCGTATGTGCTTCCAGGCGCAACAT	3205

2817 ctaccgacgctggtgctgacgacgacccctgagcttaccgtccctcccaagccacat 2876
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Db 3177 agtgtgacagctctcctcctgaaacccctgacgagcgagatcatgtatgttctg 3236
QY 3566 GCTGATACGCTGAGGCTGTTCCGATGATGAGCCCTCATCGAATCAAGCTGACCCGT 3625
Db 3237 tctgatacagcttgagcttcttgcaatgagtggtctcatctggaatcaagctgagctgt 3296
QY 3626 GCCCGTGTATCTGATCGCTTCTGTTGGCATAGAGTGAAGTTCACCGTTACGCTTGC 3685
Db 3297 gctgtgtcatcctgttctgtatctgtgtgcaatgagtgagtgatctacacgttccagctg 3356
QY 3686 TTTGGGCTTTTGTGACGCGATCGGCGACAAAGAACCGGAGGCTGTGCTTGGCTGGAAGA 3745
Db 3357 ttgagccttctgacacgcatctggaagcaagacagaggtatgctgcttgagaca 3416
QY 3746 CATGTTTGACACCCGTCGATGAGTGGCGCGCTGTCACATGCTGAGAGTCTGATGTCGC 3805
Db 3417 catgttctgctccgttctcgagcagtgctgtgtcactcgtcggtgtactagtgctgtc 3476
QY 3806 GGGATCTGAGTTGCACTTCAATGTCAGGATTTCTTGTGCTGCTGCGATCTCAACAT 3865
Db 3477 aggtccgaatttgatctatctgtcagatcttcttgcctcgtccatctctcaacgt 3536
QY 3866 CTTGGGCTTCTCAATGGGCTGGTTTGTGCTTCCGCTTGTGCTTCTTGTGGACATA 3925
Db 3537 ctgggggtctcatalgactgtgtctgtcgtctcctctatctctcttcttgagacgtg 3596
QY 3926 TCCGAGGCTGTCACGACGAGGCTTGAACCGGCTGACACCTTCCCTGAGCAGC 3985
Db 3597 tcttgagtgctcctcagcgaatgtgtcctaacacgactgccaactcctcgtcgtgagcgcc 3656
QY 3986 CCCCAGGCTGCTGCTGCTGCGCATGCGCCGCGACACGACGAGCGGCTGTGATTCCTC 4045
Db 3657 tccaagtgtcgtccgttgcgtgtccctcgtgtcacaacaaatggtgtctatctctc 3716
QY 4046 CGACTCGAGTATAGTTCCGACGACAGTAGTGTGAGGCTTCAGGAGGAGCTTGGGACATA 4105
Db 3717 cgaactcggagtagactcctcagacacagtgctgtgcatcaatgaaagatcctcaggaata 3776
QY 4106 CGAGGCGGACGAGGCGGAGGCGCTGCGCACCAAGTATGTCGGAAGCCACAGAAA 4165
Db 3777 cgaagcagcagagtggtgtcggaagcctgtcccaacaaatgtagtggaagcacaagaaa 3836
QY 4166 CCCCCTTGTGCGCACTGCTCACTGTGTCATCCGAATCCAGGACATCACCCACTCGAA 4225
Db 3837 ccctgtcttgcccgctcactgtgtctcatctcgagactcagacatcagcctccctgac 3896
QY 4226 CCGGACGACGAGCCCACTGAGACTCAAGGCTCCGTGCTCCGAGCGCAAGGCCAGCA 4285

Db 3897 cctctggaacagccccacactgagctctgtctctgtctcccttgagcgaagccagca 3956
QY 4286 GCCCGACGAGGACCCCCACGAGAAAGCTTGTGGCCACCCCTTACAGACCGGACAGAGA 4345
Db 3957 gcttcgaagagatccccctcagaagagcttggtggtccacccccctacagacggtcgagga 4016
QY 4346 CGTTTTTGAATTTCTACTGAAGGCGATTCGTGGCCTTAGCAATAGGCGCGCTGGGCGCC 4405
Db 4017 cgttttgaattctactgaagaggtatctgtccttagaataaggaacgctcgaagcc 4076
QY 4406 TCGCGGCGCGCTTCTCNCANACCCCTGGAACCCAGGCTCCACGTGCGCATGGGACACTCCCT 4465
Db 4077 ccgttggtggtccgttctcacaacccctggaacccaacgacccaacgcaatggtcagctgt 4136
QY 4466 GCCCGGCTACTGCCAGCCCATCACACTGTGAGCGGCTTGTGCTGCTGCTGCTGCTGCTGCT 4525
Db 4137 gcccaagctactgtccagcccatcaacactgtgaaggtctcgtctcgtgtgagctgtgt 4196
QY 4526 GCACCGCGCGCTGTCCCTGGGCTGGGCGGAACCCCGAGGAGACTGTGCCAG---- 4581
Db 4197 gcatcccccgt-----cctgagacctgtgcaaccccgaggggtggtccgtgtccagct 4250
QY 4582 -----GCTACCTGAGACTGACACGCGCCTGTTGAGAGACCCCACTGCTTCCACGT 4636
Db 4251 tgaagagctaccctgagactgatalcagggatattgagatctccatgtgcttctcagt 4310
QY 4637 CCGGCTGATGAGAGGAGGATTCGAGGTGGAAGTCATTTGACCTGACAGACGGAATCGGA 4696
Db 4311 caggtgtgagagagagagactcaagagtgtagatcagagctacagagagctgtgagatgta 4370
QY 4697 GGAGAGGCGCGCGGAGAGCAGCTCCAACTGAGGCTGATTAATCTGAAGCAAGAGGCC 4756
Db 4371 ggaagagcggtgtggtgagagcagctcccaactgaggttaataatctgaagcaagagcc 4430
QY 4757 AAAGATTGGAACCCCGACCCCGACCTCTTCCAGAACGCTTGAAGAGACGCTGTGG 4816
Db 4431 aaagatctggaagaa-gccgcgcgccacccctctccagaaactgtggaagagaaactgtgg 4489
QY 4817 AGTTATGGAAGAAAGATGCTCTGTGCGCAGAGCAGTTCATTTGTAACCACTGTA 4876
Db 4490 aattatgt-----ggaagcagatcatctgttaccgttaactgtatgta 4530
QY 4877 TTATTTTGTAAATATTTCTATTAATTTTAAGAGATGTACACATGTGTATATAGAGAG 4936
Db 4531 ttatctkgtgaataatctcatalaataatlaaargtgtacaca--tgaataatacagtg 4588
QY 4937 GAAGATGTAAGGTGATGATCTGGGGCTTTCACACTCCCGCCCAAGAGTGTGAGGCC 4996
Db 4589 aaatgtctgtaacgt-ctatttcttgggtccctccactcctccagagtgaggagacc 4647
QY 4997 ACAGTGGGCGCTCTCCGTAATTTGTGCAATGAGGCTCCGTCGACCAACCAAGCTTGATTTAGT 5056
Db 4648 aca--ggggccttctccctgtgtacatgtgtctgtgtgcacaacaaagcttaactag 4705
QY 5057 CTTAAA-----TTTACGACATATGTTGCTGCTCTTAAATATTTGTAATTTACTTGT 5108
Db 4706 tttaaaaaaaatctcccgacatgtgtgtgtcgtcgtcgttaataatgtlaataattactgt 4765
QY 5109 ATTAATTTGTAATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTT 5168
Db 4766 ataattctatgcaaatatgtctatglaaataagatla--tttgtaaaagttctgtttaa 4824
QY 5169 ATATTTTAATTTGATATACAAACCTGTGAGTATGTAATTTGTAATTTGTAATTTGTAATTT 5228
Db 4825 ataatttaatttgcatalcaacaacccgtgtgtagagtgatgttactcgtlaacttttg 4884
QY 5229 AACAGCTATGCGTGTATTTTGTGTTAATGAGCAGATGAGAAAGC 5280
Db 4885 aacacgctatgtgtgtlaa-----tgtttaacagagagacatgaaagaaac 4931

RESULT 6 V64092

ID	V64092	standard; cDNA; 5187 BP.
XX		
AC	V64092;	
XX		
DT	26-JAN-1999	(first entry)
XX		
DE	Mouse patched gene.	
XX		
KW	Mouse; patched gene; diagnosis; treatment; developmental disorder;	
KW	cancer; healing; injured tissue; plc; spina bifida; Wnt-1 oncogene;	
KW	sperm production; gene therapy; ss.	
XX		
OS	Mus sp.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	97..4401
FT		/*tag= a
XX		
PN	US5837538-A.	
XX		
PD	17-NOV-1998.	
XX		
PF	06-OCT-1995;	95US-0540406.
XX		
PR	06-OCT-1995;	95US-0540406.
PR	07-OCT-1994;	94US-0319745.
XX		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.	
XX		
PI	Goodrich LV, Johnson RL, Scott MP;	
XX		
DR	WPI: 1999-023461/02.	
DR	P-PSDB: W72968.	
XX		
PT	Nucleic acid encoding vertebrate patched protein and related	
PT	transformants - used to express poly(peptide)s, useful for	
PT	diagnosis and treatment of developmental disorders or cancer, and in	
PT	healing of injured tissue	
XX		
XX		
PS	Claim 1; Column 43-48; 38pp; English.	
XX		
CC	The present sequence represents the mouse patched (ptc) gene. Cells	
CC	containing and expressing the ptc gene are used for the recombinant	
CC	production of the protein. These in turn are useful: (1) for generating	
CC	antibodies (Ab); and (11) to screen for specific-binding ligands	
CC	(potential therapeutic agonists and antagonists). The ptc gene, or its	
CC	fragments, are used to isolate related sequences from other mammals; to	
CC	identify mutations (particularly those associated with genetic diseases	
CC	such as spina bifida and other developmental disorders); to monitor	
CC	expression levels in testis (to determine relationship with sperm	
CC	production) and to isolate 5'-non-coding sequences (used to study	
CC	embryonic development and to provide regulated expression of proteins).	
CC	The complete gene can be used in gene therapy, including expression of	
CC	antisense molecules, and to generate transgenic animals for studies of	
CC	embryonic development. Ab are used diagnostically to determine the	
CC	ptc protein on cell surfaces and as competitive inhibitors of signal	
CC	transduction through the ptc ligand. Cells that have been engineered to	
CC	express the ptc protein can be used to promote regrowth and healing of	
CC	damaged tissue (e.g. growth of new teeth) and regulation of the ptc	
CC	protein expression may be useful in cancer treatment (it may control the	
CC	Wnt-1 oncogene).	
XX		
XX		
50	Sequence 5187 BP; 1165 A; 1412 C; 1337 G; 1270 T; 3 other;	

Query Match	71.9%	Score	3801.2	DB	20	Length	5187
Best Local	Similarly	Pred. No.	0				
Matches	42/6	Conservative	3	Mismatches	516	Indels	57
						Gaps	11

[illegible][illegible]

QY	2306	CCCACTCCCTTACAGACCCACAGCTTTGGCCATGAAGCCAGATTACATGCAGTCCAC	2365
Db	1977	ccccaccccaatacacaacagccacagctctgcgccaaagaaacccatactcaatctgagtcac	2036
QY	2366	TGTCAAGCTCCGACGGAGTACGACCCCCACAGCCAGTGTACTACACCCCGGTGAGCC	2425
Db	2037	cgttcagctctccgcacagagatgataagccctcaacagcacggtatctaaacacccgcgcagcc	2096
QY	2426	GGCGTCCGAGATCTGTGTGACGCCCGTACACGTTGACACAGACACCCCTACAGTCCAGAG	2485
Db	2097	acgctctgagatctctgttaagccctgttaccgttcaaccagagacaacctcagctgtcaag	2156
QY	2486	CCAGAGAGACACAGCTCCACAGGGACCTGCTCTCCCAATTTCTCCAGCTCCAGCTCCCA	2545
Db	2157	tcccgagagacaagactctacacaggaacctgcctcccaattctcagactccagctccca	2216
QY	2546	CTGGCTCGAGCCCCCGTGTACGAAGTGAGACACTCTCATCTTTTGTGTAGAGACCTATG	2605
Db	2217	ctgcctccgagcccccttgacccaagtgagacactctctctgttgcagagaagacactatgc	2276
QY	2606	TGCTTTTCCTTTTAAACCAAAAGCCAAAGTATGTTGATCTTCCCTTTTCTGGGCTTGCT	2665
Db	2277	tcccttccctctcgtgaaccccaagccaaggttggtatctctcttcttctcgtgcgtgc	2336
QY	2666	GGGGGTCAAGCCTTTATGAGCACCCGAGTGAAGAGAGCGGCTGGACCTTGACGACATTGT	2725
Db	2337	gggggtcagaccttatacgtgaacaccccgagtgagagaagggctgtgaacctccgcgaacatgt	2396
QY	2726	ACCTGGGAAACCAAGAAATATGACTTTTATGCTGCACAAATTCAATACTTTTCTTTCTA	2785
Db	2397	tccccggtgaacccaagaaatalgactctcctagcttgcccagttcgaagtaacttcttctcta	2456
QY	2786	CAACATGTATATAGTACCCACAGAACACACACTACCCGAATATCCAGACACTTACTTTACGA	2845
Db	2457	caacaagtataagtaaccacgaagacagactaccggaatalaccagacacttactttagca	2516
QY	2846	CCTACACAGAGATTTCAGTAACCTGTAAGTATGTATGTTGGAGAAACAAACAGCTTCC	2905
Db	2517	ccctcaataagattctcagaacatgtgagatgatagtcagtcggtgagagaaacagaacttcc	2576
QY	2906	CAAAATGTGGCTGCACTACTTCCAGAGAGTGGCTTCAGGACCTTCAGAGTGCATTTGACAG	2965
Db	2577	ccaaatgtgtgcgtcacctactttagagacgtgtctcaaggaacttcagatgtcatttgcag	2636
QY	2966	TGACATGGGAAACCGGGAATAATGCGCAACAATTACAGAATGATGATCGACAGCATGAGCT	3025
Db	2637	tgacatgggaaactgtggagatcaatgcacaaacaattataaaatgtaacagatgcaggggt	2696
QY	3026	CCTTGCTTACAAACTCTCGTGTGCAAAACCGGACCGCGATTAAGCCCGATGCATTCAGCCA	3085
Db	2697	ccttgcttcaaaactcctgtgtgcagatcgtgcagccgagacaagcccatgacttagtca	2756
QY	3086	GTTGACTAAACGCGCTGTGTGATGCAATATGCAATGCAATTAATCCAGCGCTTTTCTACAT	3145
Db	2757	gttgcactaaacggtcgtgtgtagacgatagtgcatactaatccgagcgtcttctactac	2816
QY	3146	CTACTGTAGCGGTTTGGTTCAGCAACGACCCCTCGGTATGTGCGCTCCAGCCCAACAT	3205
Db	2817	ctactgtgacgcttgggttcagaagaacacctgttagcttgcgtctcccaagcccaact	2876
QY	3206	CCGGCCACACGACCAAGAAATGGGTCCACGACAAAGCCGACTACATGCTGTAAACAAGGCT	3265
Db	2877	ccggtcctacccggtccgaggtgtgtcatgtacacaagccgactacatgtccagagacagcgt	2936
QY	3266	GAGATTCGCGGAGAGAGGCCCATGAGATGCGCATCTCCCTTCTACTCTCAACGGGTT	3325
Db	2937	gagaaatcccaagcagacaagcccatcgagtacgctcaagttcccttctacctcaacggcct	2996
QY	3326	GCGGACACCTTCAGACTTTGTGAGGCAATTGCAAAAAGTAAGACCATCTGCAGCAACTA	3385
Db	2997	acgagacacactcagacttgtgtgaagccatagaanaaagtgagatcatctgttataacacta	3056

QY 686 CTTGGTTGTGGGCTCCTCATATTTGGGGCTTTCGCGGTGGATTAAAGCAGCGAACCT 745
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Db 357 ttgggtcgtgggtctcctcctcatttgggcttcgcgtggtgattaaagcagtaactct 416
QY 746 CGAGACCAACGTGGAGAGCTGTGGGTGAAGTTGAGAGCAGAGTAAGTCGTGAATTTAA 805
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Db 417 cggagaccaacgltggagagctgtgggtgagagltggtgagagcagtgagtcgaagattaa 476
QY 806 TTATACTCGCCAGAAATTGGAGAGGGCTATGTTTAAATCCCAACTCATGATACAGAC 865
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Db 477 ttataccgctcgaagaatcggagaagagctacgtltaactcctaactcgtatcagac 536
QY 866 CCCTAAAGAGAGAGTGTATATGTCCTGACACAGAGCGCTCTACAGACCTGTGACTC 925
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Db 537 tccaaagaagaagcgtcctaagtctctgacacagagcgtcctctgtaaacacccgtgctc 596
QY 926 GGCACCTCCAGGCGCAGCGGTGTCATATGATGATACAGAGCAGTGGAAATTTGAGACA 985
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Db 597 agcactccagagcagtcggtgacgctcactacgtltaaacagagcaatcgaagltgaaaca 656
QY 986 TTTGTGTTCAAATCGAGAGAGCTTATCCAGAGAAAGGTTACATGATGATGAATTTAGA 1045
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Db 657 ttgtgctcacaatacaggggaacttaccagagacaggttaccatggtacagataataga 716
QY 1046 ATATCTTAACTCTGTTGATTATTACACCTTTGACTGCTTCGTGGAGAGGCGGAATTT 1105
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Db 717 atacccttaccctgtcctaatacctacaccttgcgtcgtctggaagggggaagcgt 776
QY 1106 ACAGTCTGGAGAGCATCTACTCTCTAGTAAACCTCTTCGGGTGGCAAACTTCGACC 1165
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Db 777 aaagtcgagagacagctacactcctcaggaagcctccttaccggtgagcaaatcgtacc 836
QY 1166 TTTGGAATTCCTGGAAGAGTTTAAAGAAATTAACCTATCAAGTGAAGAGAGTGGAGAAAT 1225
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Db 837 ctltggaatctccagaagaaglttaagaataataactcacaagtgagacagcgtggagagaat 896
QY 1226 GGTGAATTAAGGTGAGGTGTGATGTTACATGAGACCGCCCTGCCCTCAATCCGCGCA 1285
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Db 897 gctgataaagcaggaagltggtcagatggtacatgtagacggtcgtcctaaccagcgga 956
QY 1286 TCCAACTGCCCCGCGCACAGCGCCCCCAAAAATTCACCAAACTCTTATATGAGCCCT 1345
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Db 957 cccgaatctgccttgcacagcccccatacaaaaatcacaacaaaccccttgaatgtggccct 1016
QY 1346 TGTGTTGAATGAGTGTGATGCTTATCCAGAAAGTATATGCACTGCGAGAGAGATTT 1405
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Db 1017 gtttctgaaatggtgagatgtcagagtttaccaggaagtatatgtcatltggagaagagatc 1076
QY 1406 GATTGTGGGTGGCAGATCAAGCAAGCAAGCACTGGAACACTGTCAGCGCCCATGCCCTGCA 1465
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Db 1077 gattgtgggtgtgtacacgttaagaaatgacactgtgaaactgtcagctcagcagccctgca 1136
QY 1466 GACCATGTCAGTATATGACTCCCAAGCAAAATGTACGAGCACTTCAAGGGGTAGAGTA 1525
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Db 1137 aacactgttccagttatagactcccaagaaatgtatgaacacttcaaggggtcagactta 1196
QY 1526 TGTCTACACATCAATGGAACGAGAGCAAAAGCGGACCATCTGAGAGCGCTGCGAGAG 1585
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Db 1197 tgtctcacaatcaactggaatgaaagagagcgagcgccatccctgtgagggccctggagag 1256
QY 1586 GACATATGAGAGGTGTTCAATCAGATGTCCGACAGAACTCCACTCAAAAGGTGCTTTC 1645
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Db 1257 gaactaagtcggaggtgtgtcacaaggtgtgcccccaaatcctaactcaaaaggtgtctcc 1316
QY 1646 CTTGACACACAGACCTGAGAGCATCTGAAATCCTTCTGAGAGTGAAGTCAATCCG 1705
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Db 1437 ctgctcccaagtcctccaggggtggcggtgggtgctggcgtgctgtgtgtgtgctgtcagt 1496
QY 1826 GGCCTCAGAGACTGGGCTGTGTCATGATTCGAATTTCTCTTTAAAGCTGCAACACTCA 1885
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Db 1497 ggtctggagatttggccctctgtccttctgtatgtgacatctcttctttaaagtcgtgcaactca 1556
QY 1886 GGTGTTTGCCATTTCTGCTCTGTTGGTGGTGGTGGATGATGATGATGATGATGATGAT 1945
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Db 1557 ggtttgcggttctgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1616
QY 1946 CTTCAAGTAACAGAGAGTAATTAAGATTCCTTTGAGAGAGAGAGAGAGAGAGAGAG 2005
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Db 1617 attcagtgaaacagagacagaaataaagagatcccatlttgagagagagacgtggaggtgctc 1676
QY 2006 GAAGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065
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Db 1677 caagcgacacggagcagcggtggtcctcactcactcactcactcactcactcactcactcact 1736
QY 2066 GGCCTGCTTAAATCCCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125
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Db 1737 ggcgcatltgacccctatccctgtcctcgtgagcgttctcctccagagcgtgtgtgtgtgt 1796
QY 2126 GGTGTTCAATTTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2185
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Db 1797 ggtatcaatlttgttatagtgttctgtcctatcttctcgtcaatltcctaagatgtatcata 1856
QY 2186 TCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245
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Db 1857 cagacgttgaagacagaaatltgatalatttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1916
QY 2246 AGTGAATCAGGTTTAAAGCTCCAGGCGCTTACAGCAGACAGAGAGAGAGAGAGAGAGAG 2305
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Db 1917 ggttattcaatltgtgacacagagcctcacaagagcctcacaagtaaacacgggttacaagccc 1976
QY 2306 CCCACTCTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365
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Db 1977 cccacccccatacaacagcacaagctctgcacagaaacccatatacactatgtcagttccac 2036
QY 2366 TGTCCAGCTCCGCGACAGGAGTACAGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2425
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Db 2037 cgttcagctcgcagagagatltgacccctcacaagcagcagcagcagcagcagcagcagc 2096
QY 2426 GCGCTCCGAGATCTCTGTCAGAGCGCTGACAGTGCAGAGAGAGAGAGAGAGAGAGAG 2485
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Db 2097 agcgtctgagatctctgtacagcgtgttaccgttccacagagacacacacacacacacac 2156
QY 2486 CCCAGAGAGACAGAGCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2545
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Db 2157 tcccgaagagacacagctcactacagagacgtcgtcctccagttctcagactcagactcaca 2216
QY 2546 CTGCTCGAGAGCGCCCTGTAGAGAGTGCAGACTCTCATCTTTTGTGAGAGAGAGAGAG 2605
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Db 2217 ctgctcagagccccctgacacaaagtgaacactcctcctgttctgagagagacatatgc 2276
QY 2606 TCCCTTCTCTCTTGAACCAAAAGCAAGGTAGTGTGATCTCTCTCTCTCTCTCTCTCTCT 2665
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Db 2277 tcccttctcctctgaacacacacacacacacacacacacacacacacacacacacacacac 2336
QY 2666 GGGGGGTAGCCTTTATGAGCACACCCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2725
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Db 2337 ggggtgtcagccttlatgtgacacacacacacacacacacacacacacacacacacacac 2396
QY 2726 ACCTCGGGGAAACAGAGAAATTTGACTTTATGCTGTGCAATTTCAATTTCTTTTCTTA 2785
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Db 2397 tcccgggaaacacagagataatgtacttaagctgtgcccagttcagaactcctcttcta 2456
QY 2786 CAACATGTATATAGTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2845
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Db 2457 caacatgtatatagttaccacagaaagacagactacacagatltccaagcactcacttaca 2516
QY 2846 CTTACACAGAGATTTCACTAAGTGAAGTATGTCATGTTGAGAGAGAGAGAGAGAGAG 2905
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Db 2517 cctcataaggtttccagcaatgtgaatgtatgtcatgtcgtgaggaagaacaagcaattcc 2576
Oy 2906 CAAAATGTGTGCTGACTACTTACAGAGACTGGCTTCAGGAGACTTCAGAGATGATTTGACAG 2965
Db 2577 ccaaatgtgtcgtactactcttagagactggtctcaagaagctcagaatgtacattgtacag 2636
Oy 2966 TGACTGGGAAACCGGAAATCATGTCACAAATTAACAAGAAATGATTCAGACGATGGAGT 3025
Db 2637 tgaattggaaaacttggagatcatatgcgaacaattataaataatggttcagatgaacggygt 2696
Oy 3026 CTTTGCTTACAACTCTGTTGTCAAAACCGGACCGGATTAAGCCCATGACATCAGCA 3085
Db 2697 cctcgttacaactcctcgtgtcagactcgtcagcagagaacagccatcagacattagta 2756
Oy 3086 GTTACACTAAACAGCTGTGGTGGATGAGATGAGATCATTAATCCAGGCTTCTCAT 3145
Db 2757 gtgtactaaacagcgtcgtgttagacgacagatgcatactaaacgcgtcttctacat 2816
Oy 3146 CTACCTGACGGCTTGGTTCAGACACACCCGTCGGGTATGCTGCCCTCCAGGCAACAT 3205
Db 2817 ctacttgacgcttgggttcagaaacgacctgtagctttagctgctccacagccaacat 2876
Oy 3206 CCGGACACCGACAGAAATGGGTCCACGAAAGCCGACTACATGCTTGAACAGAGCT 3265
Db 2877 ccggtcctacacggtcgtgagtggttcataatgcgaacgactacatgcagagacagact 2936
Oy 3266 GAGAAATCCGGAGAGAGGCCCATGAGATGATGCCAGTTGCCCTTTCACCTCAACGGGTT 3325
Db 2937 gagaatcccaacagacagagcccaatgcgaatgcgtcagttcccttctacatcaagcgtc 2996
Oy 3326 GCGGACACCTCAGACTTGTGTGAGCAATTGAAAAATTAAGACCATCTGCACAGACTA 3385
Db 2997 acgagacaccttcagacttgtgtgaagccatagaaaagtgaagtcactgttaacacta 3056
Oy 3386 TACGAGCCTGGGGCTGTGCAGTTACCCCAAGGCTACCCCTTCTCTTGGGAGCACTA 3445
Db 3057 tacagactgtgagactgtcagatcccaatgcgtaccccttccgtctcgtgtgagacata 3116
Oy 3446 CATGGGCTCCGCACTGGCTGCTGTGTTTCACTGATGATGATGATGATGATGATGATGAT 3505
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Oy 3506 CGTGTGCGCTGTCTCTTCTGTAACCCCTGAGACGCGCGGATCATTTGTGATGTTCTGGC 3565
Db 3177 agtgtgacagcttctcctcctcgtacgtacgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 3236
Oy 3566 GCTGATGACGTCGAGCTGTTGGGCAATGATGGGCTTCATGGAATCAAGCTCAGTGGCGT 3625
Db 3237 tctgatacgttctgacttctgtgcatgtatggtcctcatctggaatctcaagctgactgct 3296
Oy 3626 GCGGCTGGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3685
Db 3297 gctgtgtgtacatcctgtatgtcatctgtgtgcacgtgagatgtatccgtccacgtgtgc 3356
Oy 3686 TTTGGGCTTCTGACGCGCATGCGGCAAGAACCGGAGGCTGTGGCTTGGCTGGAGCA 3745
Db 3357 ttgtgccttctgtacagcatttgggagaaagaacacagagctatgtcgtcgtcgtcgtcgt 3416
Oy 3746 CATGTTTGCACCGCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3805
Db 3417 catgttctcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 3476
Oy 3806 GGAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3865
Db 3477 aggtgtcgaattgtatctatgtcagatctccttgcgtcgtcgtcgtcgtcgtcgtcgtcgt 3536
Oy 3866 CCTCGGCTTCTCAATAGGCGTGTGTTGCTTCCGCTGCTTGTGTTGTTGTTGTTGTTGTTGTT 3925
Db 3537 ctgtgggtgtcctcaatgtgactgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 3596
Oy 3926 TCCTAGAGTGTCTCCAGGCAAGGCTTGAACCGCTTCACACACCTCCCTGAGCCAC 3985

Db 3597 tctgtagtggtctccagccaatgtgctaaacgactgtccacitcctcgtcgtcgtcgtcgtc 3656
Oy 3986 CCCGAGCGGTGTCCGCTTGCCTGATGCGCGCCGCGCACACGAGCGGCTGTGATTCCTC 4045
Db 3657 tccaagtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 3716
Oy 4046 CGACTGCGAGTATGTTTCCACAGACAGTGTCAAGGCTTCAGGAGAGCTTCGGCACTA 4105
Db 3717 cgactcgtgagtagactcctcagaccacgtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 3776
Oy 4106 CGAGGCCCGAGGCGGCGGAGGCGCTGCGCCACCAAGTATGTTGGAAGCCACAGAAA 4165
Db 3777 cgaagcaacagaggtgtcgtgaggtccctgcacacaaagtgtgtgtgtgtgtgtgtgtgtgt 3836
Oy 4166 CCCGCTTGTGCGCACTGCTGATGCTCATCCGAAATTCAGAGCATCCACCTCGAA 4225
Db 3837 cctcgttcttgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 3896
Oy 4226 CCCGAGACAGACCGCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4285
Db 3897 cctcgtcgaacagcccaactgtgactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 3956
Oy 4286 GCGCGGACAGGACCCCGCCAGAGAGGCTTGTGGCCACCCCTTACAGACCGCGCAGAGA 4345
Db 3957 gctcgtgaaggtatccctcagaaaggtcgtggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 4016
Oy 4346 CGCTTTGAAATTTCTACTAAGGGCATTCGTGCGCTACGAATAGGGCGCTGGGGCC 4405
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Oy 4406 TCGGGGGGCGCTTCTCACAACCTCGGAACCCAGCTTCACCTGCGATGGGACGCTCGCT 4465
Db 4077 ccgtgtggtccgttctcactacacccctgcgaacacagctccacgcgtcgtgagagctgtgt 4136
Oy 4466 GCGGCTTACTGTCAGCGCCATCACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 4525
Db 4137 gccacgtactgtccagccatcaccactgtgtgaggtcgtcgtcgtcgtcgtcgtcgtcgtcgt 4196
Oy 4526 GCACCCGCGCGCTGTCCCTGGGCTGTGGGCGGAGCCCGGAGGGGACTGTGCCAG--- 4581
Db 4197 gcatcccccgt-----cctgacactgtgtgcgaaccccgaggggtccctgtcaggtta 4250
Oy 4582 -----GCTACCCGTGAGCTGACACAGCGCTTTGTGAGGACCCCGACGTCCTTCCACT 4636
Db 4251 tgaagactacccctgagactgtatcaggggtatcttgaagatccctcgtcgtcgtcgtcgt 4310
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Db 4311 caggtgtgagagagaggaactcaaaagtgtgaggtcatagagctacagagcgtgtgaatgtga 4370
Oy 4697 GGAGAGGCGCCGGGGAAGCAGCTCCAACTGAGGATTAATTAATCTGAAGCAAGAGGCC 4756
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1077 gatttgtagtgatccctcaagaaatgcacactlbgaaactlbgcagcgctcaacgcttga 1136
1466 GACCATGTCCAGTTAATGACTCCCAAGCAATGTACGAGCACTTCAAGGGATCAGATA 1525
1137 aaccatgctcaatcaatgactcccaagaaatgataatgaaacttcaaggggtcaacta 1196
1526 TGTCTCAGCTCACTCACTGGAACGAGACAAAGCGGCGCCATCTTGAGGCGCTGGAGAG 1585
1197 tgcctcacaactcaactlgaatgaagacagcgccgcacatccctggaagcctlbgcagag 1256
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1826 GCGTCGACGAGCTGGCTGCTGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885
1497 ggcgcagagatlggcccctctgctctctgctlgtcagtgctlgttcaatgctlbgcagaa 1556
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1946 CTTCAGTAAACAGACAGAAATTAAGAAATCCCTTTGAGAGACAGACCGGCGGCTGCT 2005
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2426 GCGCTCCGAGATCTCTGTGACAGCGCTGACGCTGACAGACAGACACCTGACGCTGACGAG 2485
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 QY 4763 TGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4822
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 QY 4823 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4882
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 Db 4772 caatgcaaatatgtctatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 4830
 QY 5175 TAAATTTGATATACACACCTGCTGATGATGAATATTTAGTGTGATGATTTTCAAGACAG 5234
 Db 4831 taattgtatatacaaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4890
 QY 5235 CTATGCGTATATTTTGTGTTAATGAGCAGATATGAAGAAAGC 5280
 Db 4891 ctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4950

RESULT 10
 ID 231717 standard; DNA; 4030 BP.
 XX 231717;
 DT 19-JAN-2000 (first entry)
 DE Human patched-2 coding sequence.
 KW Patched-2; p14; human; signalling molecule; hedgehog cascade; stroke;
 KW cell proliferation; cell differentiation; testicular cancer; gut disease;
 KW degenerative disorder; nervous system disorder; Parkinson's disease;
 KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
 KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
 KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
 KW therapy; ss.
 OS Homo sapiens.
 XX
 XX W09953058-A1.
 XX
 XX 21-OCT-1999.
 XX
 XX 02-APR-1999; 99WO-US07417.
 XX
 XX 15-APR-1998; 98US-0060939.
 XX

PA (GETH) GENENTECH INC.
 XX De Sauvage FJ, Carpenter DA;
 XX WPI, 1999-620428/53.
 DR P-PSDB; Y43261.

XX New isolated human patched-2 gene, used to develop products for
 PT treating, e.g. cancer and Alzheimer's disease -
 XX
 PS Claim 1; Fig 1; 124pp; English.

XX This sequence encodes the human patched-2 (ptch-2) protein of the
 CC invention. The patched-2 polypeptides are signalling molecules,
 CC specifically for signalling and mediator molecules in the hedgehog (hh)
 CC cascade which are involved in cell proliferation and differentiation.
 CC They can be used for the treatment of disorders which are mediated at
 CC least in part by hh, especially Dhh, e.g. testicular cancer. They can
 CC also be used for treating degenerative disorders of the nervous system,
 CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou
 CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
 CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
 CC diseases, skin diseases, diseases of the testis (including infertility),
 CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
 CC osteoporosis. Antagonists or agonists of patched-2 may be used for
 CC treating disorders or creating a desirable physiological condition
 CC effected by blocking hh signalling, especially Dhh signalling,
 CC e.g. contraception or infertility treatment. The products can also be
 CC used for detection, diagnosis, drug screening and production of
 CC transgenic animals.
 XX

SQ Sequence 4030 BP: 728 A; 1297 C; 1141 G; 864 T; 0 other;

Query Match 22.2%; Score 1176.4; DB 20; Length 4030;

Best Local Similarity 61.5%; Pred. No. 7.9e-245;
 Matches 2058; Conservative 0; Mismatches 1221; Indels 69; Gaps 8;

QY 591 GCTACTGCGGCGAAGCGCAGCTGTCGAGAGCGAAGTTGAGAGACTTATTTAAA 650
 DB 311 gctgagagcctgaagctcactctgctcgtctactcagagcctctcct 370
 QY 651 CTGGGTTTACATTCMAAATAAACTGCGCAAGTTCTTGTTGGCCCTCTATATTT 710
 DB 371 ctggatcgagatccagagcaatctggaagtgctctctcgtgagctctg 430
 QY 711 GGGGCTTCGCGGTGGGATTTAAAGACGAGCACTGAGCAACAGGAGAGAGCTGG 770
 DB 431 ggggcccgtgcatctgagctcgcagatctatctatctgagacaactctggaacgctctg 490
 QY 771 GTGGAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
 DB 491 gtgagagtgagagagagagagagagagagagagagagagagagagagagag 550
 QY 831 GAGGCTATGTTTAACTCACTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 551 gaggctgcatcactcagatctgatacagcagcagcagagagagagagagagag 610
 QY 891 CTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 950
 DB 611 ctcaacccagagcactctgagcctcagcagcagcagcagcagcagcagcagcag 670
 QY 951 GTATACATGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
 DB 671 gtatacctatctgagagagcctgagagagagagagagagagagagagagag 730
 QY 1011 ATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
 DB 731 ctatctgaaatgagatgagatgagatgagatgagatgagatgagatgagatg 790
 QY 1071 ACACCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
 DB 791 accccctcagatctctctgagagagagagagagagagagagagagagagagag 850

QY 1131 GGTAAACCTCTTGGGCTGGAGCAAACTTGACCTTTGGAAATCTGAGAGATTAAAG 1190
 DB 851 ggcgcgcccagatcaccagtgagagagagagagagagagagagagagagagag 910
 QY 1191 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1250
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 QY 1251 GGTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
 DB 968 gctcagtgagagagagagagagagagagagagagagagagagagagagag 1027
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 DB 1028 aaccatacagagagagagagagagagagagagagagagagagagagagagag 1087
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 DB 1088 ttctccacaatctcagatctgagagagagagagagagagagagagagagagag 1147
 QY 1431 AGCACTGGAATACTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1490
 DB 1148 ccccaagagagagagagagagagagagagagagagagagagagagagagag 1207
 QY 1491 AAGCAATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1550
 DB 1208 cgcagctgagagagagagagagagagagagagagagagagagagagagag 1267
 QY 1551 GACAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1610
 DB 1268 gagcagagcagagagagagagagagagagagagagagagagagagagag 1327
 QY 1611 AGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1670
 DB 1328 gcccctcagagagagagagagagagagagagagagagagagagagagagag 1387
 QY 1671 ATCCTGAATTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1730
 DB 1388 atctgagatgctctcagagagagagagagagagagagagagagagagagag 1447
 QY 1731 CTGGCTATGCTGTCATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1790
 DB 1448 ctggcctatgagagagagagagagagagagagagagagagagagagagagag 1507
 QY 1791 GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1850
 DB 1508 ggccttgagagagagagagagagagagagagagagagagagagagagagag 1567
 QY 1851 TTGATCGAATTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1910
 DB 1568 ctgctgagagagagagagagagagagagagagagagagagagagagagag 1627
 QY 1911 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1970
 DB 1628 atcggcgtgagagagagagagagagagagagagagagagagagagagagag 1681
 QY 1971 AGAATCCCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2030
 DB 1682 ggcacccctcagagagagagagagagagagagagagagagagagagagagagag 1741
 QY 2031 CTACAGTCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2090
 DB 1742 ctacacatcacaacacacacacacacacacacacacacacacacacacacac 1801
 QY 2091 CTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2150
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 QY 2151 CTGATTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2210
 DB 1862 ctgctctcagagagagagagagagagagagagagagagagagagagagagag 1921

RESULT 12
 A09081
 ID A09081 standard; cDNA; 3453 BP.
 AC A09081;
 XX 10-AUG-2000 (first entry)
 XX Human patched-like gene (PTCH2) coding sequence.
 DE
 XX Patched 2, PTCH2; tumour suppressor; familial melanoma CMM1;
 KW familial adenomatous polyposis; hMOM; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; gene therapy; chromosome 1p32-35; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 13..3453
 FT /*tag= a
 PN MO200020037-A1.
 XX 13-APR-2000.
 XX 06-OCT-1999; 99WO-SE01784.
 XX 06-OCT-1998; 98SE-0003393.
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
 PI Hollingsworth RE;
 XX
 DR WPI: 2000-303645/26.
 DR P-SDSB: Y92225.
 XX
 PT Isolated human protein capable of participating in human patched
 PT gene/Sonic hedgehog pathway during embryonic development is used in
 PT medication for treatment of condition involving tumors such as basal
 PT cell carcinoma
 XX
 XX
 PS Claim 4; Page 45; 55pp; English.
 XX
 CC This cDNA is derived from the novel human patched 2 gene (PTCH2), which
 CC has been localised by radiation hybrid mapping to chromosome 1p32-35
 CC with DIS211 and W1404 as closest flanking markers and with an estimated
 CC localisation 5.5 cR from DIS443. This region is often lost by LOH in
 CC various different tumour types, such as neuroblastoma, melanoma and
 CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
 CC gene in this region. It is also a candidate gene for involvement in
 CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
 CC hMOM1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
 CC exist (see A09082-84). PTCH2 is capable of participating in the human
 CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent.
 CC
 XX
 SQ Sequence 3453 BP; 600 A; 1135 C; 989 G; 729 T; 0 other;
 Query Match 22.2%; Score 1171.6; DB 21; Length 3453;
 Best Local Similarity 61.4%; Pred. No. 8,1e-244;
 Matches 2055; Conservative 0; Mismatches 1224; Indels 69; Gaps 8;
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 DB 91 gctggagcgccgaagcctccactcgtctgtctactcaggccgctctctct 150

QY 651 CTGGCTTGTACATTCAAAAAACTGCGCAAGTTCCTGGTGTGGCCCTCCATATTT 710
 DB 151 ctggggtgcgagctccagagacatctgagcaagtgctctctcggagccttgcctt 210
 QY 711 GGGGCTTCGCGGTGGATTAAAGCAGCAACCTCGAGACACACGCGGAGCTGG 770
 DB 211 ggggcccctggcattaggtccgcattcgcattatcgagcaaacctggacaagctcgt 270
 QY 771 GTGGAAGTTGAGAGAGAGTAAAGTCTGTAATTAATTAATCTGCGCAAGATTGAGAA 830
 DB 271 gtagaagtgaggcagccgggtgagccagagctgcatlaccaagagagagctgggag 330
 QY 831 CAGGCTATGTTTAATCTCAACTCATGATATACACCCCTTAAGAAAGAGTGTAAATGTC 890
 DB 331 gaggctgataaacctcattagatgatacaagcagcagcagagagagagagaaacatc 390
 QY 891 CTGACACAGAGCGCTCTACACACCTGAGCTCGACCTCCAGCGAGCGGTGTCAT 950
 DB 391 ctcaacaccggaagcaacttggcctccacctccagcagccctcaactgcaagtaagctcaa 450
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 DB 451 gtatcacctctagggagctcgtgagattgaaacaaatcgtacaaagtcagagagctccc 510
 QY 1011 ATCAGAGAAGAGGTTTACATGATCAGATTAATTAATTAATCTTACCTGTTGATTAAT 1070
 DB 511 ctatctgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 570
 QY 1071 ACACCTTTGAGCTGCTTCTGGAGAGGCGCAATTAAGTCTGGAGACAGCTTACCTCTTA 1130
 DB 571 accccctcgaactgctctcctggagagagagagagagagagagagagagagagagagagag 630
 QY 1131 GGTAAACCTCTCTGGGTTGGAGCAACCTTGACCTTTGGAATTCGTGAAGAGTTAAAG 1190
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 QY 1371 TTATCCAGAAAGATATATGACCTGGCAGAGAGAGTGTATTTGGGTGGCAGACTCAAGAAC 1430
 DB 868 ttctcccaaaaattcatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 927
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 DB 1108 ggcctgcctgagagagccttccagcagatcagatcagatcagatcagatcagatcagatcag 1167
 QY 1671 ATCTGAAATCTTCTCTGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1730
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 QY 1731 CTCGCTATGCTGTCTAATCAATGCTGCGCTGGAGACTGCTCAAGTCCAGAGGTCCGCTG 1790

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:14:57 ; Search time 116.97 Seconds
(without alignments)
7285.763 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288
Sequence: 1 GAATTCGGGAGCCGCAAGG.....TATGAAGAAAGCCCGGAATT 5288

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 segs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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5: /cgn2_6/prodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5288	100.0	5288	2	US-08-540-406-18
2	5288	100.0	5288	3	US-08-656-055-18
3	5288	100.0	5288	4	PCT-US95-13233-18
4	3801.2	71.9	5187	2	US-08-540-406-3
5	3801.2	71.9	5187	2	US-08-540-406-9
6	3801.2	71.9	5187	3	US-08-656-055-3
7	3801.2	71.9	5187	3	US-08-656-055-9
8	3801.2	71.9	5187	4	PCT-US95-13233-3
9	3801.2	71.9	5187	4	PCT-US95-13233-9
10	411.8	7.8	3900	2	US-08-356-0608-42
11	411.8	7.8	3900	2	US-08-460-900C-42
12	405	7.7	4434	2	US-08-540-406-5
13	405	7.7	4434	3	US-08-656-055-5
14	405	7.7	4434	4	PCT-US95-13233-5
15	405	7.7	4434	4	US-08-540-406-7
16	77	1.5	345	2	US-08-656-055-7
17	77	1.5	345	4	PCT-US95-13233-7
18	67.6	1.3	4524	2	US-08-845-988-7
19	67.6	1.3	4524	2	US-09-206-537-7
20	66.6	1.3	736	2	US-08-540-406-1
21	66.6	1.3	736	2	US-08-540-406-1
22	66.6	1.3	736	4	PCT-US95-13233-1
23	64.8	1.2	8438	1	US-07-945-283-1
24	61	1.2	397	3	US-09-253-691-3
25	60.8	1.1	6530	2	US-08-146-930-1
26	60.8	1.1	6530	3	US-08-458-240-1
27	60.8	1.1	6530	4	PCT-US93-03993-1
28	60.4	1.1	5115	3	US-08-348-518C-3

C 29	60.4	1.1	5115	3	US-08-476-509B-3	Sequence 3, Appl1
C 30	58.8	1.1	5288	2	US-08-540-406-18	Sequence 18, Appl1
C 31	58.8	1.1	5288	3	US-08-656-055-18	Sequence 18, Appl1
C 32	58.8	1.1	5288	4	PCT-US95-13233-18	Sequence 18, Appl1
C 33	57.6	1.1	1235	2	US-08-557-309B-53	Sequence 53, Appl1
C 34	57.6	1.1	2144	3	US-08-834-306-15	Sequence 15, Appl1
C 35	57.4	1.1	530	3	US-08-758-662-4	Sequence 4, Appl1
C 36	57.4	1.1	4257	2	US-08-690-473-1	Sequence 1, Appl1
C 37	57.4	1.1	5117	3	US-08-854-585-1	Sequence 1, Appl1
C 38	57.4	1.1	5117	4	PCT-US95-05512-1	Sequence 1, Appl1
C 39	57.4	1.1	12001	1	US-08-458-568A-11	Sequence 11, Appl1
C 40	56.8	1.1	234	1	US-08-469-802B-3	Sequence 3, Appl1
C 41	56.8	1.1	234	2	US-08-267-803B-3	Sequence 3, Appl1
C 42	56.8	1.1	2823	1	US-08-398-008A-1	Sequence 1, Appl1
C 43	56.8	1.1	2823	2	US-08-893-333-1	Sequence 1, Appl1
C 44	56.4	1.1	2538	3	US-08-899-437-1	Sequence 1, Appl1
C 45	56.4	1.1	10348	2	US-08-457-273B-41	Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-08-540-406-18
; Sequence 18, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-540-406-18

Query Match 100.0%; Score 5288; DB 2; Length 5288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGAGCCGCAAGAGTGGCGGGAAGCGCCGGAAGAGAGCTCGCTGGCGC 60
DB 1 GAATTCGGGAGCCGCAAGAGTGGCGGGAAGCGCCGGAAGAGAGCTCGCTGGCGC 60

OY	61	GC	GGCTCTCGCTCTTCCGCGCACTGATGTGGCAGCGCGCGCGCGCAGACACTTCGGGA	120
Db	61	GC	CGCTCTCGCTCTTCCGCGCAACTGGATGTGGGACGCGCGCGCGCAAGACTTCGGGA	120
OY	121	CCCCGCGCAATGTGGCAATGGAAGCGCAGGGTCTGACTTCCCGGCACGGCCCGCGGC	180	
Db	121	CCCCCGCGCAATGTGGCAATGGAAGCGCAGGGTCTGACTTCCCGGCACGGCCCGCGGC	180	
OY	181	GCAGCGCAGCAGCGCCCGCGCTGTGAGCAGCAGCAGCGCGCTGTCTGTCAACCGGAGCC	240	
Db	181	GCAGCGCAGCAGCGCCCGCGCTGTGTAGCAGCAGCAGCGCGCTGTCTGTCAACCGGAGCC	240	
OY	241	CGAGCCCGGAGCGCTCGCGCGCAGCAGCGCTCTCGCAACCCGACCGCCAGCGGCCCAAG	300	
Db	241	CGAGCCCGGAGCAGCTCGCGGCCACGACGCTCTCTGCAACCCGACCGCCAGCGGCCCAAG	300	
OY	301	GAGCCCGCAGCAGCGCGCAGCAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360	
Db	301	GAGCCCGCAGCAGCGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360	
OY	361	CGCGCGCGCGCGCGCGCGCGCGCAACATGCGCTCGGTGTAACGCGCGCGAGCGCCAGGACC	420	
Db	361	CGCGCGCGCGCGCGCGCGCGCGCAACATGCGCTCGGTGTAACGCGCGCGAGCGCCAGGACC	420	
OY	421	CGCGCGCGCGCGCGCAGCGCGCTGTATCGTGTGCCCGGAGCGCGCGCTGAGGCGGAGGC	480	
Db	421	CGCGCGCGCGCGCGCAGCGCGCTGTATCGTGTGCCCGGAGCGCGCGCTGAGGCGGAGGC	480	
OY	481	GCAGACGCAACGGGGGGGGCTGCCCGCTGTCTGCGCGCGCGCGGCACTATCTGACCGGC	540	
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OY	541	CCAGCTACTGCAACGCGCGCTTCTGCTGTGGAGAGATTTTCAAGGGGGAAGGCTACTGGCC	600	
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OY	601	GGAAAGCGCACTGTGGCTGTAGAGCAGATTTAGAGACTCTTATTTTAACTGGGTGTT	660	
Db	601	GGAAAGCGCGCACTGTGGCTGTAGAGCAGATTTTAGAGACTCTTATTTTAACTGGGTGTT	660	
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Db	721	CGGTGGATTTAAAAAGCAGCGCAACCTCTGAGACCAACCTGTGAGAGCTGTGGGTGGAAGTTG	780	
OY	781	GAGGACGAGTAAGTGTGAATTAATTAATTAATCTGCGCCAGGAAGTTGGAGAGAGGCTATGT	840	
Db	781	GAGGACGAGTAAGTGTGAATTAATTAATTAATCTGCGCCAGGAAGTTGGAGAGAGGCTATGT	840	
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Db	841	TTTAATCTCAACTCATGATACAGACCCCTTAAGAGAAGGCTAATGTCTTGACACAG	900	
OY	901	AACCGCTCCACAAACACCTGAGACTCGGCACTCCAGGCGACCGGTCTCATGTATACATGT	960	
Db	901	AACCGCTCCACAAACACCTGAGACTCGGCACTCCAGGCGACCGGTCTCATGTATACATGT	960	
OY	961	ACAACAGGCGAGTGGAAATTTGGAACATTTGTTCACAAATCAGGAGACTTATCACAGAAA	1020	
Db	961	ACAACAGGCGAGTGGAAATTTGGAACATTTGTTCACAAATCAGGAGACTTATCACAGAAA	1020	
OY	1021	CAGGTTACATGATCAGATTAATGAATATCTTTTACCCTTGTGTGATTAATTAACACTTTGG	1080	
Db	1021	CAGGTTACATGATCAGATTAATGAATATCTTTTACCCTTGTGTGATTAATTAACACTTTGG	1080	
OY	1081	ACTGCTTCTTGGAAGGGGCGCAATTAAGTCTGGGAAGAGATACCTCTCTAGATTAACCTC	1140	
Db	1081	ACTGCTTCTTGGAAGGGGCGCAATTAAGTCTGGGAAGAGATACCTCTCTAGATTAACCTC	1140	
OY	1141	CTTTCGGGTGGACAAACTTGACCCCTTTGGAAATTCCTGGAAGACTTAAGAAATTAAC	1200	

Db	1141	CTTTCGGGTGGACAAACTTCGACCTTTGGAAATTCCTGGAAAGTTAAAGAAATAAAT	1200
Qy	1201	ATCAAGTGGACAGCTGGGAGGAAATGCTGAATPAAGCTGAGTTGGTCAATGCTTACATGG	1260
Db	1201	ATCAAGTGGACAGCTGGGAGGAAATGCTGAATPAAGCTGAGTTGGTCAATGCTTACATGG	1260
Qy	1261	ACGGCCCCCGCTCAATCCGGCGATATCCAGACTGGCCCCGCCACAGCCCCCAACAAAATT	1320
Db	1261	ACGGCCCCCGCTCAATCCGGCGATATCCAGACTGGCCCCGCCACAGCCCCCAACAAAATT	1320
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Qy	1381	AATATATGACATGGCAGAGGAGATGATTTGGTGGGCACAGTCAGAAACAGACTGGAA	1440
Db	1381	AATATATGACATGGCAGAGGAGATGATTTGGTGGGCACAGTCAGAAACAGACTGGAA	1440
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Db	1441	AACTGGTCAGGCCCATATGCCCTTGACAGACCATGTTCCAGTTAATGACTCCCAAGCAAAATG	1500
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Db	1501	ACGAGCACTTCAAGGGGTACGAGATATGTCTACACACATCAACTGGAAACGAGNCAAAAGCG	1560
Qy	1561	CAGCCATCCTGGAGGCGCTGGCAGAGAGACATATGTGAGAGTGGTTCAATCAGATGTGGCAC	1620
Db	1561	CAGCCATCCTGGAGGCGCTGGCAGAGAGACATATGTGAGAGTGGTTCAATCAGATGTGGCAC	1620
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Qy	1681	CCCTTCGTAGCGTCACTGTACATCCGGGTGGCCAGCGGCTACTTACATCATCTGGCTATG	1740
Db	1681	CCCTTCGTAGCGTCACTGTACATCCGGGTGGCCAGCGGCTACTTACATCATCTGGCTATG	1740
Qy	1741	CCGTGCTAACCATGCTGCGGTGGGACTGCTCAAGTCCAGGCTGCCGTGGGCTGGCTG	1800
Db	1741	CCGTGCTAACCATGCTGCGGTGGGACTGCTCAAGTCCAGGCTGCCGTGGGCTGGCTG	1800
Qy	1801	GGGTCTGCTGGTGTGACATGTACGTAGGTGACAGAGTCCAGAGTCCGGGCTGTGCTCAATTCGGAA	1860
Db	1801	GGGTCTGCTGGTGTGACATGTACGTAGGTGACAGAGTCCAGAGTCCGGGCTGTGCTCAATTCGGAA	1860
Qy	1861	TTTCCCTTAAAGCTGCAACAACTCAGGTTTTGCCATTTCGCTGTTGGTGGTGGTG	1920
Db	1861	TTTCCCTTAAAGCTGCAACAACTCAGGTTTTGCCATTTCGCTGTTGGTGGTGGTG	1920
Qy	1921	ATGATGTTTTCTTCTTGCGCCAGCCGCTTCAGTAAACAGGACAGAAATPAAGAAATCCCTT	1980
Db	1921	ATGATGTTTTCTTCTTGCGCCAGCCGCTTCAGTAAACAGGACAGAAATPAAGAAATCCCTT	1980
Qy	1981	TTGAGGACAGGACCGGGGAGTGGCTGAAGCGCAACAGAGGACAGAGTGGCCCTCAGTCCA	2040
Db	1981	TTGAGGACAGGACCGGGGAGTGGCTGAAGCGCAACAGAGGACAGAGTGGCCCTCAGTCCA	2040
Qy	2041	TCAGCAATGTCAACAGCTTCTTATGCGCGCGTTAAATCCCAATTCGCGCTGTGGGGCGT	2100
Db	2041	TCAGCAATGTCAACAGCTTCTTATGCGCGCGTTAAATCCCAATTCGCGCTGTGGGGCGT	2100
Qy	2101	TTACCCCTCCAGGACGGGTAGTATGTGTTTCAATTTTGGCATATGTTCTGCTCAATTTTTC	2160
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RESULT 2
 US-08-656-055-18.
 Sequence 18, Application US/08656055
 Patent No. 6027862
 GENERAL INFORMATION:
 APPLICANT: SCOTT, MATHEW P
 APPLICANT: GOODRICH, LISA V
 APPLICANT: JOHNSON, RONALD L
 TITLE OF INVENTION: Patched Genes and their Use
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/656,055
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/540,406
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: a60190-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-396-3249
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-656-055-18

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QY 3841 TTGCTGTGCTGGAGATTCCTCACCATTCCTGGGGCTTCATGATGGGCTGTTTGTCCCG 3900
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QY 3901 TGCCTTTGTCTTTTGGAGCATATCTGAGGTGTCTCCAGCAAGGCTTGAACGCC 3960
Db 3901 TGCCTTTGTCTTTTGGAGCATATCTGAGGTGTCTCCAGCAAGGCTTGAACGCC 3960
QY 3961 TGCCTTTGTCTTTTGGAGCATATCTGAGGTGTCTCCAGCAAGGCTTGAACGCC 4020
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QY 4081 GCCTGAGGAGAGGCTTGGGCTTACGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4140
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QY 4201 AATCCAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4260
Db 4201 AATCCAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4260
QY 4261 TGCCTCCGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCT 4320
Db 4261 TGCCTCCGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCT 4320
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Db 4561 CCGGAGGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4620
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Db 4621 ACCTGCTTCCAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCT 4680
QY 4681 AGGAGCTGAGATGAGGAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4740
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QY 4741 CTGAGCAAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4800
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Db 4801 GAAAGAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCC 4860
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QY	4921	TGTGTAATATAGGAGAGAGATGTAAGTGTATGATCTGGGGCTTCTCCACTCCGCC	4980
Db	4921	TGTGTAATATAGGAGAGAGATGTAAGTGTATGATCTGGGGCTTCTCCACTCCGCC	4980
QY	4981	CCAGAGTGTGGAGCCACAGTGGGGCCCTCTCCGATTTGTGTGATTTGGGCTCCGTGCCACA	5040
Db	4981	CCAGAGTGTGGAGCCACAGTGGGGCCCTCTCCGATTTGTGTGATTTGGGCTCCGTGCCACA	5040
QY	5041	ACCAAGCTTCATTAAGTCTTAATTTTCAGCATATGTGTGCTGCTGCTTAATATTTGTATTAAT	5100
Db	5041	ACCAAGCTTCATTAAGTCTTAATTTTCAGCATATGTGTGCTGCTGCTTAATATTTGTATTAAT	5100
QY	5101	TTACCTGTGTAATATTCATATGCAAAATATTCGCTATGTAAATAGATTTATTTGTAAAGTTTC	5160
Db	5101	TTACCTGTGTAATATTCATATGCAAAATATTCGCTATGTAAATAGATTTATTTGTAAAGTTTC	5160
QY	5161	TGTTTAAATATTTTAAATTTTGCATATACACAACCTGTGTGTAGTATGAATGTTACTGT	5220
Db	5161	TGTTTAAATATTTTAAATTTTGCATATACACAACCTGTGTGTAGTATGAATGTTACTGT	5220
QY	5221	AACCTTCAACACGCTATGGGTGATTAATTTTCTTTATATGAGCATATGGAAGAAC	5280
Db	5221	AACCTTCAACACGCTATGGGTGATTAATTTTCTTTATATGAGCATATGGAAGAAC	5280
QY	5281	CCGGAAT 5288	
Db	5281	CCGGAAT 5288	
RESULT 3			
PCT-US95-13233-18			
: Sequence 18, Application PC/TUS9513233			
: GENERAL INFORMATION:			
: APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY			
: TITLE OF INVENTION: Patched Genes and their Use			
: NUMBER OF SEQUENCES: 19			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert			
: STREET: Four Embarcadero Center, Suite 3400			
: CITY: San Francisco			
: STATE: CA			
: COUNTRY: US			
: ZIP: 94111			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.30			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: PCT/US95/13233			
: FILING DATE: 06-OCT-1990			
: CLASSIFICATION:			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Rowland, Bertram I			
: REGISTRATION NUMBER: 20015			
: REFERENCE/DOCKET NUMBER: a60190-1			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 415-781-1989			
: TELEFAX: 415-398-3249			
: INFORMATION FOR SEQ ID NO: 18:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 5288 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: cDNA			
PCT-US95-13233-18			
Query Match 100.0%; Score 5288; DB 4; Length 5288;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY	1	GAATTTCCGGGGACCCCAAGAGATGCGCGCGGAAGCCGCCCAAGAGACAGGCTCGTCGGCG	60
Db	1	GAATTCGGGGACCCCAAGAGATGCGCGCGGAAGCCGCCCAAGAGACAGGCTCGTCGGCG	60
QY	61	GCCGGCTCTCGCTCTTCGCGGAAGTGGAGGACGGCGCGCCAGAGACCTCGGA	120
Db	61	GCCGGCTCTCGCTCTTCGCGGAAGTGGAGGACGGCGCGCCAGAGACCTCGGA	120
QY	121	CCCCGGCCAAATGTGGCAATGGAAGCGGAGGGTCTGACTCCCCGGCAGCGGGCGCGGC	180
Db	121	CCCCGGCCAAATGTGGCAATGGAAGCGGAGGGTCTGACTCCCCGGCAGCGGGCGCGGC	180
QY	181	GCAGCGGACAGCAGCCGCCCGCTGTGTAGCAGCAGCAGCGAGGCTGTGTTCACCGGAGCC	240
Db	181	GCAGCGGACAGCAGCCGCCCGCTGTGTAGCAGCAGCAGCGAGGCTGTGTTCACCGGAGCC	240
QY	241	CGAGCCCGCAGCAGCTCGCGGCCAGCAGCGTCTCTCGCAAGCCGACGCCCCAGCGCGCCAG	300
Db	241	CGAGCCCGCAGCAGCTCGCGGCCAGCAGCGTCTCTCGCAAGCCGACGCCCCAGCGCGCCAG	300
QY	301	GAGCCCGCAGCAGCGGACACAGCGCGCGCGGCCGCCGGGAAACCTCTCCGCCGCGCGG	360
Db	301	GAGCCCGCAGCAGCGGACACAGCGCGCGCGGCCGCCGGGAAACCTCTCCGCCGCGCGG	360
QY	361	GCGGCGGCGGCGCGCGGCAACATGGCCTCGGCTGTGTAAAGCGCGCCGAGCCCCAGAGCC	420
Db	361	GCGGCGGCGGCGCGCGGCAACATGGCCTCGGCTGTGTAAAGCGCGCCGAGCCCCAGAGCC	420
QY	421	GGGGGGGGGGGGGCGGCGGCTGTATCGGTGGCCCCGGGAGCGCGCGGTGGAGGGGGAGGC	480
Db	421	GGGGGGGGGGGGGCGGCGGCTGTATCGGTGGCCCCGGGAGCGCGCGGTGGAGGGGGAGGC	480
QY	481	GCAGACGAGCGGGGGGGGCTGCGCGCTGTCTGCTGCAGCGCGGAGCCGGAGCTATCTGCACCGC	540
Db	481	GCAGACGAGCGGGGGGGGCTGCGCGCTGTCTGCTGCAGCGCGGAGCCGGAGCTATCTGCACCGC	540
QY	541	CCAGCTACTGCGCACGCGCGCTTCTGCTGTGGAGCAGATTTCCAAAGGGGAGGCTACTGCGC	600
Db	541	CCAGCTACTGCGCACGCGCGCTTCTGCTGTGGAGCAGATTTCCAAAGGGGAGGCTACTGCGC	600
QY	601	GGAAGCGCGACCTGTGGCTGTGAGAGCCAAAGTTTACAGACTCTTATTTAACTGGAGTTGTT	660
Db	601	GGAAGCGCGACCTGTGGCTGTGAGAGCCAAAGTTTACAGACTCTTATTTAACTGGAGTTGTT	660
QY	661	ACATTCAAAAAAATCTGCGGCAAGTTCTTGTGGTGTGGGCTCTCATATTTTGGGCGCTTCG	720
Db	661	ACATTCAAAAAAATCTGCGGCAAGTTCTTGTGGTGTGGGCTCTCATATTTTGGGCGCTTCG	720
QY	721	CGGTGGGATTAAGAGGAGCAACCTGGAAGCCAAAGTGGAGGAGCTGTGGGTGGAACATTG	780
Db	721	CGGTGGGATTAAGAGGAGCAACCTGGAAGCCAAAGTGGAGGAGCTGTGGGTGGAACATTG	780
QY	781	GAGGACGAGTAAGTCGTGTAATTAATTTACTCGCCAGAGATTTGGAAGAGAGGCTATGT	840
Db	781	GAGGACGAGTAAGTCGTGTAATTAATTTACTCGCCAGAGATTTGGAAGAGAGGCTATGT	840
QY	841	TTAATTCCTAACTCATGATACGAGACCCCTTAAGAAAGAGTGTCTATGTCTGACACAG	900
Db	841	TTAATTCCTAACTCATGATACGAGACCCCTTAAGAAAGAGTGTCTATGTCTGACACAG	900
QY	901	AAGCGCTCTTACAAACACCTGTGACCTGCGCACTCCAGGCGACCGGTGTCAATGTATACATGT	960
Db	901	AAGCGCTCTTACAAACACCTGTGACCTGCGCACTCCAGGCGACCGGTGTCAATGTATACATGT	960
QY	961	ACAACAGCGAGTGGAAATTTGGAACATTTGTTTACAATCAGAGAGCTTATACAGAAAA	1020
Db	961	ACAACAGCGAGTGGAAATTTGGAACATTTGTTTACAATCAGAGAGCTTATACAGAAAA	1020
QY	1021	CAGGTTCACATGATCGATCAATTAATGATATCTTACCTGTTGTGATATATACACTTTGG	1080
Db	1021	CAGGTTCACATGATCGATCAATTAATGATATCTTACCTGTTGTGATATATACACTTTGG	1080

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1141 CTTTGGGAGTGGACAACTTGGACCTTTGGATTCTGGAGAGTAAAGAAATTAACCT 1200
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 Qy 4141 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4200
 Db 4141 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4200
 Qy 4201 AATTCAGGATCAACCTCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4260
 Db 4201 AATTCAGGATCAACCTCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4260
 Qy 4261 TGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4320
 Db 4261 TGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4320
 Qy 4321 CACCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4380
 Db 4321 CACCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4380

Qy 4381 CTAGCAATAGGGCCCGCTGGGGCCCTGCGGGGGCCCGTTTCTACAAACCTCGGAACCCAG 4440
 Db 4381 CTAGCAATAGGGCCCGCTGGGGCCCTGCGGGGGCCCGTTTCTACAAACCTCGGAACCCAG 4440
 Qy 4441 CGTTCACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4500
 Db 4441 CGTTCACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4500
 Qy 4501 CTTCCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4560
 Db 4501 CTTCCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4560
 Qy 4561 CCGGAGGGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4620
 Db 4561 CCGGAGGGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4620
 Qy 4621 ACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4680
 Db 4621 ACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4680
 Qy 4681 AGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740
 Db 4681 AGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740
 Qy 4741 CTGAGCAAAAGAGCCCAAGATTGTGAAACCCCAACCCCACTTTTCCAGAACTGCTT 4800
 Db 4741 CTGAGCAAAAGAGCCCAAGATTGTGAAACCCCAACCCCACTTTTCCAGAACTGCTT 4800
 Qy 4801 GAGGAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4860
 Db 4801 GAGGAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4860
 Qy 4861 ACTGTACCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
 Db 4861 ACTGTACCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
 Qy 4921 TGTGTATATATGGAAGAGATGTAAAGTGTATGTGTGTGTGTGTGTGTGTGTGT 4980
 Db 4921 TGTGTATATATGGAAGAGATGTAAAGTGTATGTGTGTGTGTGTGTGTGTGTGT 4980
 Qy 4981 CCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5040
 Db 4981 CCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5040
 Qy 5041 ACCAAGCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5100
 Db 5041 ACCAAGCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5100
 Qy 5101 TTACTTGTATATATGCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5160
 Db 5101 TTACTTGTATATATGCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5160
 Qy 5161 TGTGTAAATATATTTAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5220
 Db 5161 TGTGTAAATATATTTAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5220
 Qy 5221 AACTTCAAAACGCTATGCGGATATTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
 Db 5221 AACTTCAAAACGCTATGCGGATATTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
 Qy 5281 CCGGAATTT 5288
 Db 5281 CCGGAATTT 5288

RESULT 4
 US-08-540-406-3
 ; Sequence 3, Application us/08540406
 ; Patent No. 5837538
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V

[illegible]

QY	3146	CTACCTACAGCGCTTTGGGTTCAGCAACGAGCCCGTGCGTATCTCGCTTCGCCACAGCCACAT	3205
Db	2817	CTTACTTTCACCGCTTTGGGGTCACAGCAACGACCCCTGTAGCTTACCGTGCCTCCACGGCCACAT	2876
QY	3206	CCGGCCACACGACGACAGATATGGATGATCCAGCAAAAGCCGACATACATAGCTTGTGAACAGGCT	3265
Db	2877	CCGGCCCTCACCGCGCGGAGTGGATGTCATGACAAAGCCGACATACATGCCAGAGACCGAGCT	2936
QY	3266	GAGAAATCCCGGACAGAGAGCCCATCGAATATGCCAGTTCCTCTTCTCACTCAACGGGT	3325
Db	2937	GAGAAATCCCGAGACAGAGAGCCCATCGAATAGCTAGTTCCTCTTCTCACTCAACGGCT	2996
QY	3326	GGGGAGACACCTCGAGACTTTTGGGAGGGCAATTGAAAAAGTAAAGACCATCTCGACACATA	3385
Db	2997	ACGAGACACCTCGAGACTTTTGGGAGGGCAATTGAAAAAGTAAAGTAAAGTAACTCTTACACATA	3056
QY	3386	TACGAGCCTGGGGGTGTCCAGATTACCCCAACGAGCTACCCCTCTCTCTGTGGAGGACATA	3445
Db	3057	TACGAGCCTGGGAGCTGTCCAGATTACCCCAATAGGCTTACCCCTCTCTCTGTGGAGGACATA	3116
QY	3446	CATCGGCTCCGGCCACTGCGTGCCTGCTGCTTCATCAGCGTGGTGTGGCGCTGCACATTCT	3505
Db	3117	CATCAGCGCTCGGCCACTGCGTGCCTGCTATCATCAGCGTGGTGTGCCTGCCTCACGTTTCT	3176
QY	3506	CGTGTGCGCTGTCTTCCTTCTGAAACCCCTGGAGCGCGGGATCTATTGATGGTCTGCG	3565
Db	3177	AGTGTGCGCAGTCTTCTCCTCTGAACCCCTGAGCGCGGGATCTATTGATGGTCTGCG	3236
QY	3566	GCTGATGACGCGTGAAGCTGTTGGGACATATGGGCGCTCATCGAATCAAGCTCAATGTGCGCT	3625
Db	3237	TCGATGACCGCTTGAGCTCTTTGGACATATGGGCGCTCATTTGGGATCAAGCTGAATGCTGT	3296
QY	3626	GGCCGTGATCATCTGATGCGCTCTGTGGCCATATAGAGATGGAGTTACCGTTACGTTTC	3685
Db	3297	GCGTGTGGTATCTCTGATTCATCTGTGGCATGTGGAGTGGAGTCAACCGTCAACGTGCG	3356
QY	3686	TTTTGCGCTTTCTGACGGCCATCGCGCGACAAAGACCGAGGGGCTGTGCTTCCCGTGGAGCA	3745
Db	3357	TTTTGCGCTTTCTGACAGCCATTGGGGACAAAGAACACAGGGCTATGCTGCCCTCTGGAGACA	3416
QY	3746	CATGTTTGGACCCGCTCGATATGGGCGCGTGCCTCACTCTGCTGGAGTGGTATGCTGAGC	3805
Db	3417	CATGTTTGGTCCCGTCTCGAGCGTCTGTGCCTCTGCTCACTGCTCGGTGATGATGCTTGC	3476
QY	3806	GGGATTCGATTCGACTTCATTTCTCAAGATTTCTTGTGCTGCTGGCCGATTCGCAACAT	3865
Db	3477	AGGGTCCGAATTTGATTTATTTCTAGATTAATCTTTGCCGCTCTGGCCATTTCTACCGT	3536
QY	3866	CGTCGGCGCTTCATATGGGCTGCTTTTGTCTCCGTCGCTTTGTCTTTTGGACATA	3925
Db	3537	CTTTGGGGGTTCTCAATGAGCACTGGTTCGTGCTCTGCTCTTATCCCTTCTTTGGACGTTG	3596
QY	3926	TCTCTAGGATGTCTCAGCCACAGCGGCTTGAACCGCTGCGCCACACCCCTCCGCTAGGCAC	3985
Db	3597	TCTCTAGGATGTCTCAGCCCAATGGGCTTAAACGACACTGCCACTCTTCCGCTTAGAGCGCC	3656
QY	3986	CCCCAGCGTGGTCCGCTTGCATGCGCGCCCGGCGACACGACAGCGGGCTTCATTCTCTC	4045
Db	3657	TCTCAAGTGTCCGCTGGTTCGCGTGCCTCTGTGCTCACAGAACATATGGGTGATTTCTCTC	3716
QY	4046	CGACTTCGGAGTATGATTTCCACAGACGACATGTATAGGCGCTCAGAGAGAGCTTGGCAGTA	4105
Db	3717	CGACTTCGGAGTACACTCTCACAACACGCGTGTCTGGCATCAAGAGAGACTCAAGGCAATA	3776
QY	4106	CGAGGCCACAGCGGCGCGGGAGGCCCTGCCACCAAGTATCTGGAAGCCACAGAAAA	4165
Db	3777	CGAAGCACAGCGGCGCGGAGGCCCTGCCACCAAGTATTTGGAGAGCCACAGAAAA	3836
QY	4166	CGCGCTTTTTCGCGCCATCCAGTGTGGTCCATCCCGAATCCAGGCATCACCCACCTCGAA	4225
Db	3837	CGCTGTCTTTTTCGCGCGGTCCACTGTGTGCTCATCCGACTTCACAACATCACCTCTCTTGAC	3896

QY	4226	CCCGAGACAGCAGCCCCACCTGAGATCTAGGGGCGCTGCGCTCCCGGACGGCAAGGGCAGCA	4285
Db	3897	CCCTTCGGCAAGAGCCCCACCTGGACTCTGGCTCTCTTTCCTTCCCTGGACGGCAAGGCCAGCA	3956
QY	4286	GCCCCGCAGGGAGCCCCCGCCAGAGAGGGCTGTGGGCGACCCCTCTACAGACCGCGCAGAGA	4345
Db	3957	GCTCTGAGAGGATGCCCTTAGAGAAAGGGCTGGGGCGACCCCTTACAGACCGCGCAGAGA	4016
QY	4346	CGCTTTGAAATTTCTACTGAAAGGCAATTCCTGGCCCTAGCAATATAGGGCCCGCTGGGGCCC	4405
Db	4017	CGCTTTTGAATTTCTACTGAAAGGGCAATTCCTGGCCCTAGCAATATAGGGACCGCTCAGGGCC	4076
QY	4406	TGCGGGGGCGCGCTTCTCACAACCTTCGGAACCCAGGGTCCAGCTGCATGGGCAAGTCCCGT	4465
Db	4077	CCGTGGGGCGCGCTTCTCACAACCTTCGGAACCCAGGGTCCAGCTGCATGGGCAAGTCCCGT	4136
QY	4526	GCACCGCGCGCGCTGTGCCCTGGGGCGTGGGGGGGAACCCCGAGGGGGAGCTCGGCCAG----	4581
Db	4197	GCATCCCCG-----CTTGGACTGTGGGCGCAACCCCGAGGGGGCGCTGTCCAGGCTA	4250
QY	4582	-----GCTACCCCTGAGACTGACACAGGCGCTGTTTGAAGAACCCCGACGTGCTTTCCAGCT	4636
Db	4251	TGAGAGCTACCTCGACACTGATCAGCGGGGTATTTGAGAGATCCCAAGTGCCTTTTATGCT	4310
QY	4637	CCGGTGTGAGAGAGGAGGATTCGAAGGTGGAAGTCATTGGAGTCGACAGAGCTGGAAATGCGA	4696
Db	4311	CAGGTGTGAGAGAGGAGGACTCCAAAGGTGGAGGTCAATAGACTACAGAGAGCTGGAAATGTGA	4370
QY	4697	GGAGAGGCCCCGGGGGAAGCAGCTCCAACTGAGGGGTATTTAAATCTGAAAGCAAGAGGCC	4756
Db	4371	GGAGAGGCGCGTGGGGGAGCAGCTCCAACTGAGGGGTATTTAAATCTGAAAGCAAGAGGCC	4430
QY	4757	AAAGATTGGAACCCCCACCCCGCTCTTCCACAACCTGGAAGAGAACTGGTTGG	4816
Db	4431	AAAGATTGGAAGAA--GCCCGCGCCCGCCACTCTTCCAGAAGCTGTGAAGAGAACTGGTTGG	4889
QY	4817	ACTTATGAGAAAGATGCCCGTGCACAGCAGCAGTTCATTGTTACTGTAACGATTTGTA	4876
Db	4490	AATTATG-----GGAAGGCAGTTCAATTGTTACTGTAACGATTTGTA	4530
QY	4877	TTATTTTGTAAATATTTTCTATATAATATTTTAAGAGATGTACACATGTGTATATAGAGAG	4936
Db	4531	TTATTTTGTAAATATTTTCTATATAATATTTTAARAGGTGTACACA--TGTAATATACATGG	4588
QY	4937	GAGGAGTGTAAATGTGGATATCATCTGGGGCGTCTTCACATCTCGCCCGAGAGTGTGGAAGCC	4996
Db	4589	AAATGCTGTACAGT--CTATTTCTCTGGGGCGCTCTCCACTCCTGCCCGAGAGTGGGAGACCC	4647
QY	4997	ACAGTGGGGCGCTTCGCTATTTGTGCAATTTGGGGCTCGGTGCCACACCAAGCTTCATTAGT	5056
Db	4648	ACA--GGGGCGCTTCCCGCTGTACTATTTGGTCTCTGTGCACACCAAGCTTAACTTAG	4705
QY	5057	CTTTAAA-----TTTCCACATATGTTGCTGCGGTCTTAAATATTTGTAATAATTTACTTGT	5108
Db	4706	TTTTTAAAAAAATCTCCACACATATGTGCGTGGCTTAAATATTTGTAATAATTTACTTGT	4765
QY	5109	ATATACTATGCAAAATATTCCTATGTATGATATGATATTTTGTAAAGGTTTCTGTTTAA	5168
Db	4766	ATATTTCTATGCAAAATATTCCTATGTATGATATGATATGATATGATATGATATGATATGAT	4824
QY	5169	ATATTTTAAATTTGCATATACACAACCCGTGGTGTAGTATGAATGTTCATGTTAACTTTCA	5228
Db	4825	ATATTTTAAATTTGCATATACACAACCCGTGGTGTAGTATGATGTTTACTGTTAACTTTTG	4884
QY	5229	AACAGCTATGCGGATATATTTTGTGTTTAAATGAGAGATGATGAAAGAAC	5280
Db	4885	AACAGCTATGCGGTGTA-----TTGTTTAAAGCAGCAGACATGAAAGAAAC	4931

Query Match	71.9%	Score 3801.2	DB 2	Length 5187
Best Local Similarity	88.1%	Pred. No. 0		
Matches 4276	Conservative	3	Mismatches 516	Indels 57
			Gaps	11
446	CGGTGCCCCGGGACGGCGCTGTGAAGCGCGGAGCGCAGACGAGCGGGGGCTGCGCG	505		
120	CGGGGCGCTGGCGCAGGACGCGCGCGCGCGGAGCGGCACAGCGACCGGCGACCCACCG	179		
506	TGCTGCGCGCGCGGACCGGACTATCTGTGACCGGCGCCACTGCTGGAGCGCGCGCTGCG	565		
180	C---GCCGGCGCGGACCGGAGCTATCTGTGACCGGCGCCACTGCTGGAGCGCGCGCTGCG	236		
566	TCTGAGCAGATTTCCAAAGGGGAGGCTACTGCGCGGAAAGCGCCACTGTGGCTGAGAGC	625		
237	TCTGGAGCAGATTTCCAAAGGGGAGGCTACTGCGCGGAAAGCGCCACTGTGGCTGAGAGC	296		
626	GAGTTTCAGAGACTCTTATTAACTGGGTTGTATCAATTCAAAAAACTGGGGCAAGTT	685		
297	GAGTTTCAGAGACTCTTATTAACTGGGTTGTATCAATTCAAAAAACTGGGGCAAGTT	356		
686	CTTGGTTGGGGCGCTCATATTTGGGGCGCTCGCGGTGGGATTTAAAGCAGCAAGCT	745		
357	TTTGGTTGGGGCGCTCATATTTGGGGCGCTCGCGGTGGGATTTAAAGCAGCAAGCT	416		
746	CGAGACCAACGTGAGAGACTGTGGGTGGAAGTTGGAGGACGAGTAAGTGTGATTTAA	805		
417	CGAGACCAACGTGAGAGACTGTGGGTGGAAGTTGGGTGGAAGTGTGATTTAA	476		
806	TTTACTCGCCAGAAATTTGGAGAAAGGCTATGTTAATCTCAACTATATGATTAAGAC	865		

Db	4 177	TTATATCCCGTCAAGAATAGGAGAAGAGCTATGTTTAATCCTCAACATCATGATACAGAC	536
Qy	866	CCCTAAGAAGAAGGTGCTAATATGTCCTGACCAACAACCGCTCCATCAACACCTGAGACTC	925
Db	537	TCCAAAAGAAGAGCGCTAATATGTTCTTACCCACAGAGGCTCTCTCGCAACACTGGAGCTC	596
Qy	926	GGCACTCCAGGCCACGCCCTGTCATGTAATACATGTAACAACAGGCAAGTGGAAATTGGAAACA	985
Db	597	AGCACTCCAGGCGCAGTCTGTGCAACGTCCTCATGTATTAACAGGCAATGGAAGTTGGAAACA	656
Qy	986	TTTGTGTTACAAATCAGAGAGAGCTTATCAGAGAAACAGTTCACATGCAATGCAATATATGA	1045
Db	657	TTTGTGCTACAAATCAGGGGAACCTTATCAGGAGACAGAGTACATATGATCAAGATTAATGA	716
Qy	1046	ATATCTTATACCCTTGTGTTGATTATTAACCTTTTGAGCTCTTCTGGGAAGGGCGAAATT	1105
Db	717	ATACCTTTTACCTTGTCTTAATCATTTAACCCTTTGAGCTGCTTCTGGGAAGGGCAAGCT	776
Qy	1106	ACACTGTGGGACACATACCTCCATAGGTAACACCTCTTGCGGTGGAGCAACCTTCGACC	1165
Db	777	ACAGTCCGGGACAGCATATCCTCTTAGGTAGCCCTCTTACGGGTGCAACCTTTGACCC	836
Qy	1166	TTTGGAAATTCCTGGAAGATTAAAGAAATTAACATCAAGTGGACAGCTGGAGAGAAAT	1225
Db	837	CTTGGAAATTCCTAAGAAAGTTAAAGAAATTAACATCAAGTGGACAGCTGGAGAGAAAT	896
Qy	1226	GCCTGAATAAGGCTAGAGTGGTGTATGTTTACATGAGACCGCCCTGCTCAATCCGGCCGA	1285
Db	897	GCCTGAATAAGCCGAAATGGCATGGGTACATGAGACCGGCGCTTGCTCAACCCAGCCGA	956
Qy	1286	TCCAGACTGCCCGCCACAGCCGCCCAACAAAAATTCAACCAACCTTATATATGAGCCCT	1345
Db	957	CCGAGATTTGCCCTTGCCACACGCCCTTACAAAAATTCAACCAACCTTATATGAGCCCT	1016
Qy	1346	TGTTTTGAATGGGAGATGTCATGGCTTATATCAGAAATATATGCACTGGCAGAGAGATT	1405
Db	1017	TGTTTTGAATGGTGGATGTCTCAAGGTTTATCAGAGAAATATATGCAATTGGCAGAGAGATT	1076
Qy	1406	GATTGTGGGTGGACAGATCAAGAAACAGCACTGGAAAACTGTGAGCGCCCATGCCCTGCA	1465
Db	1077	GATTGTGGGTGGTACCGTCAAGAAATGCCACTGGAAAACTGTGAGCGCTACGCCCTGCA	1136
Qy	1466	GACCATGTTCCACTTATATGACTCCCAAGCAAAATGTACAGACACTTCAAGGGGTACAGATA	1525
Db	1137	AACCATGTTCCACTTATATGACTCCCAAGCAAAATGTATGAACACTTCAAGGGGTACACACTA	1196
Qy	1526	TGTCTCACACATCACTGNAACAGAGACAAGAGGGAGCCATCTGAGAGGCTGGAGAG	1585
Db	1197	TGTCCTCACATCACTGGAATGAACAGGCGCAGCCGCCATCTGAGAGGCTGGAGAG	1256
Qy	1586	GACATATGTGGAGTGGTTTCATCAGAGTGTGCACAGAACTCCACTCAAAAAGGTGCTTTC	1645
Db	1257	GACTTACGTGGAGGTGGTTTCATCAAAAGTGTGCCCCAAACTCCACTCAAAAAGGTGCTTTC	1316
Qy	1646	CTTGCACACAGAGACCTCTGAGAGCACTCTCGAATCCCTCTGAGTCAGTCAATCCG	1705
Db	1317	CTTGCACACAGAGACCTCTGAGAGCACTCTTAATATCTTCTGTATGTCAAGTCAATCCG	1376
Qy	1706	CCTGGCAGAGGCTACTTACTATGCTCGCTATGCTGTCTTAACCATCTCGCGTGGGA	1765
Db	1377	ACTGGCAGAGGCTACTATGCTATGCTGTCTGTATGCTTTTAACCATCTCGCGTGGGA	1436
Qy	1766	CTGTCTCAAGTCCCAAGGGAGCCGTGGGGTGGCTGGCGTCCGCTGGTGGCACTGTCACT	1825
Db	1437	CTGTCTCAAGTCCCAAGGGAGCCGTGGGGTGGCTGGCGTCCGCTGGTGGCACTGTCACT	1496
Qy	1826	GGCTCAGAGACTGGGCCCTGTGCTCAATGATCGGAATTTCCCTTAAACGTCAAACAATCA	1885
Db	1497	GGCTCAGAGATTTGGGCCCTGTGCTCTCTTATTTGGCAATTTCTTTAATGCTCGCAACAATCA	1556
Qy	1886	GGTTTTGCATTTCTCGGCTCTTGGGTGGTGGTGGATATGTTTTTCTTCTGSCCAAGC	1945
Db	1557	GGTTTTGGCCTTTCTTGTCTTTGGTGGTGGTGGATATGTTTTCTTCTCTGSCCAAGC	1616

QY	1946	CTTCAGTAAACAGCAGCAAGATTAAGAAATCCCTTTTGAGGACAGAGCCGGGAGTGCCT	2005
Db	1617	ATTTCAGTAAACAGCAGCAGAAATTAAGAGATTCCATTTTGAGGACAGAGCTGGGGAGTGCCT	1678
QY	2006	GAAAGCGCAGAGAGCCACCGAGGCCCTCACGTCCTATGACAAATGTGCACAGCCTTCCTCAT	2065
Db	1677	CAAGCGCACCGGAGCCACGCGTGGCCTCACCTCCATCAGCAATGTGCACCGCCTTCCTCAT	1736
QY	2066	GGCGCGTTAATCCCAATTTCCCGCTCTTGCGGGAGCGTTTCCCTCCAGGAGCGGTAGT	2129
Db	1737	GGCGCGAATTGATCCCTATCCCTGCGCCCTCGAGCGGTTCCTCCAGCGCTGCTGTGTGTGT	1796
QY	2126	GGTGTCAAAATTTGGCAGATGGTTCGTCATATTTTCTCTGCAATTTCTCAGCATGATTTATA	2185
Db	1797	GGTATTCAATTTTGTATGGTTGTGTGCTCATTTTTCCTGCAATTTCTCAGCATGATTTATA	1856
QY	2186	TCGACGGCAGAGACAGGAGACTGGAATTTTTCGTGTGTTTTCAGAGCCCTCGACAGAG	2245
Db	1857	CAGACGCTGAGAGCAGAGAATTTGGATTTTTCGTGCTGTTTCCAAAGCCCTGTGTACAGAG	1916
QY	2246	AGTATTCAGGTTAAACCTTAGGCTTACACCAGACACAGCACAATACCCGCTACAGCC	2305
Db	1917	GGTATTCAAGTTTAGCGCACAGGCCCTACACAGACCTCTACAGTAAACCCCGTACAGCC	1976
QY	2306	CCGACCTCCGTACAGCAGCCACACCTTTGGCCATGAAACCGAGATTCACATGACGTCCAC	2355
Db	1977	CCGACCCCGCATACACAGCCACAGCCTTCGCCACGAATCCCATATCACTATGACGTCCAC	2036
QY	2366	TGTCCAGCTCCGACGGAGTACGACCCCCACAGCCAGCAGTGTACTACACCAACCGCTGAGCC	2425
Db	2037	CGTTCACGCTCCGACAGAGTATGACCTCTCACACGACGAGTGTACTACACCAACCGCGAGCC	2096
QY	2426	GGCGTCCGAGATCTCTGTGAGCCCGTACCGGTGACACAGACACCCCTACGCTGCCAGAG	2485
Db	2097	ACGCTCGAGATCTCTGTACAGCCTGTTACCGTTCACCCAGAGACAACTCAGCTGTCCAGAG	2156
QY	2486	CCGAGAGACACACAGCTTCCAAAGGAGCGTCTCCAGATTCTCCGACATCCAGCCGCCA	2545
Db	2157	TCCCGAGAGACACAGCTCTACAGGAGCACGCTCTCCAGTCTCAGAGCTCCAGCGTCCA	2216
QY	2546	CTGCTCTGAGACCCCGCTGTACGAAGTGGAGACACTCATCTTTTGTGTGAGAGCACTATGCG	2605
Db	2217	CTGCTCTGAGACCCCGCTGTACGAAGTGGAGACACTCTCTTTTGTGACAGAGACACTATGCG	2276
QY	2606	TCTTTCTCTTGAACCAAAAGCCAAAGGTAGTGTATCTTCTTTTGTGGCTGTGCT	2665
Db	2277	TCTTTCTCTCTGAACCAAAAGCCAAAGGTGTGTATCTCTTTTCTTGTGGCTGTGCT	2336
QY	2666	GGGGGTGAGCCTTTATGGGACCAACCCGAGTGAAGAGACGGGCTGACCTTATCGCAATTTGT	2725
Db	2337	GGGGGTGAGCCTTTATGGGACCAACCCGAGTGAAGAGACGGGCTGACCTTATCGCAATTTGT	2396
QY	2726	ACCTGGGAAACCCAGAAATATGACTTTTATTTGTGACAAATTCAAATACCTTTCTTTCTTA	2785
Db	2397	TCCCGCGGAAACCCAGAAATATGACTTTTATTTAGCTGCCAGTTCAATCTCTCTTTCTTA	2456
QY	2786	CAACATGTATATAGTACACCCAGAAACCAACACATACCCGAATATTCAGCACTTACTTTAGCA	2845
Db	2457	CAACATGTATATAGTACACCCAGAAACCAACACATACCCGAATATTCAGCACTTACTTTAGCA	2516
QY	2846	CCTACACAGAGTTTCAGTACGCTGAAGTATGTATGTGGAAGAAACAAACAGCTTCC	2905
Db	2517	CTTCATTAAGATTTTCAGCAATGTGAATGTATGTATGCTGTGAAGAGAACACAGCACTTCC	2576
QY	2906	CAAAATGTGCGTCACTACTTTAGAGACTGTGCTTCAAGGACTTTCAGAGATGTCAATTTGACAG	2965
Db	2577	CCAAATGTGCGTCACTACTTTAGAGACTGTGCTTCAAGGACTTTCAGAGATGTCAATTTGACAG	2636
QY	2966	TGACTGGGAAACCGGGAAATATCATCCCAACCAATTTACAAATGGATATGACAGATGGAGT	3025
Db	2637	TGACTGGGAAACCGGGAGATCATCCCAACCAATTTATATAAATGTATGATGACAGGGGT	2696

Dh 180 C---GCCGCCGCGACCGGACTATCTGCCGCCCGACCTACTGCGACCGCCCTTCC 236
Qy 566 TCTGAGCAGATTTCAGAGGGAGGCTACTGCGGGAAGGCGCACTGGCTGAGAC 625
Dh 237 TCTGAGCAGATTTCAGAGGGAGGCTACTGCGGGAAGGCGCGCTGGCTGAGAC 296
Qy 626 GAAGTTTCAGAGACTCTTATTTAACTGGGTGTTACATTTCAAAAACCTGGCGCAAGTT 685
Dh 297 GAAGTTTCAGAGACTCTTATTTAACTGGGTGTTACATTTCAAAAAGAACTGGCGCAAGTT 356
Qy 686 CTGGGTGTTGGGCTTCCCTCATATTGGGGCTTCGCGGTGGGATTAAAGCAGCAACT 745
Dh 357 TTTGTTGTTGGGTCTCCCATATTGGGGCTTCGCTGGGATTAAAGCAGCAACTATCT 416
Qy 746 CGAGCCAGCTGGAGAGCTGGGTGAAGTTGGAGAGCAGTAAAGTCGTAATTA 805
Dh 417 CGAGCCAGCTGGAGAGCTGGGTGAAGTTGGAGAGCAGTAAAGTCGTAATTA 476
Qy 806 TTATCTCGCAGAGATTGGAGAGGCTATGTTTAACTCACTCATGATACAGAC 865
Dh 477 TTATCCCGTCAGAAATAGGAGAGGCTATGTTTAACTCACTCATGATACAGAC 536
Qy 866 CCTTAAGAAAGAGTGTCTATGCTCTGACACAGAGGCTCTTCAACACTGAGCTC 925
Dh 537 TCCAAAAGAAAGAGGCTTAATGTTCTGACACAGAGGCTCTTCAACACTGAGCTC 596
Qy 926 GGCACTCCAGGCGACCGCTGTCATGTATACATGTACACAGGCAAGTGAATTTGAGCA 985
Dh 597 AGCACTCCAGGCGACCTGTCTGTCACGTCTACATGTATACAGGCAAGTGAATTTGAGCA 656
Qy 986 TTTGTTTACAATTCAGAGAGAGCTTATCAGAGAAACAGTTACATGATCAGATAATAGA 1045
Dh 657 TTTGTTTACAATTCAGAGAGAGCTTATCAGAGAAACAGTTACATGATCAGATAATAGA 716
Qy 1046 ATATCTTACCTTGTGTTGATTTATACACTTTGGAGCTGCTCTGGGAAGGGCGAATT 1105
Dh 717 ATACTTATACCTTGTGTTGATTTATACACTTTGGAGCTGCTCTGGGAAGGGCGAATT 776
Qy 1106 ACAGTCTGGAGAGCATCTCTAGTAACTCTTGGGAGTGAACAACTTCAGACC 1165
Dh 777 ACAGTCCGAGAGCATCTCTAGTAACTCTTGGAGTGAACAACTTCAGACC 836
Qy 1166 TTTGGAATTCCTGAGAGATTAAAGAAATTAACATCAAGTGGAGAGCTGGAGAAAT 1225
Dh 837 CTGGAATTCCTGAGAGATTAAAGAAATTAACATCAAGTGGAGAGCTGGAGAAAT 896
Qy 1226 GCTGAATTAAGGCTGGAGTGGTGCATGTACATGGAGCGCCCTGGCTCAATCCGCCCA 1285
Dh 897 GCTGAATTAAGGCTGGAGTGGTGCATGTACATGGAGCGCCCTGGCTCAATCCGCCCA 956
Qy 1286 TCCAGACTGCCCCGCGACAGCCCCCAACAAATTCACCAAACTCTTGATATGGCCCT 1345
Dh 957 CCCAGATTGCCCTGCGCACAGCCCCAACAATAATTCACCAAACTCTTGATATGGCCCT 1016
Qy 1346 TGTTTTGAATGGTGCATGTATGCTTATCCAGAAAGTATATGCACTGGCAGAGAGATT 1405
Dh 1017 TGTTTTGAATGGTGCATGTATGCTTATCCAGAAAGTATATGCACTGGCAGAGAGATT 1076
Qy 1406 GATTGTGGTGGCAGAGTCAAGCAAGCAGTGGAAACCTGCAAGGCGCCATGCCGCA 1465
Dh 1077 GATTGTGGTGGTACCGTCAAGAAATGCTGGAATACTGTCAGGCTCACGCCCTGCA 1136
Qy 1466 GACCATGTTCCAGTTAATGACTCCCAAGCAATGTACAGCACTTCAAGGGATACAGTA 1525
Dh 1137 AACCATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTACAGGGGCTACAGACTA 1196
Qy 1526 TGTCTACACATCAACTGGAACGAGACAAAGCGGCACTCTGGAGGCTGGAGAG 1585
Dh 1197 TGTCTCTACATCAACTGGAATGAGACAGGCGGCACTCTGGAGGCTGGAGAG 1256
Qy 1586 GACATATGTGAGGTGTTGATCAGAGTGTGCGACAGAACTCCACTCAAAAGTGTCTTC 1645
Dh 1257 GACTTACGTGAGGTGTTGATCAAAAGTGTGCGCCCAAACTCCACTCAAAAGTGTCTTC 1316

Qy 1646 CTTCACACACAGACCCCTGGAGCAGATCTGAATTCCTCTGACGTCAGTGTATCCG 1705
Dh 1317 CTTCACACACAGACCCCTGGAGCAGATCTGAATTCCTCTCTGATGTACATGTATCCG 1376
Qy 1706 CGTGGCCAGCGGCTTACTCATGCTGCGCTATGCTGTCTAACAGATGTCGCGGGA 1765
Dh 1377 AGTGGCCAGCGGCTTACTCATGATGTGCTGATGCTGTAACTGATGCTGCGGGA 1436
Qy 1766 CTGCTCCAAATCCCAAGGTCGCGTGGGCTGGGCTGCGCTGCTGCTGCTGCTGCT 1825
Dh 1437 CTGCTCCAAATCCCAAGGTCGCGTGGGCTGGGCTGCGCTGCTGCTGCTGCTGCT 1496
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Dh 1497 GGCCTGACAGACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
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Dh 1677 CAAGCCGACGAGAGCCAGCGCTGACAGCTTCATCAGCAATGTCACAGCCTTTCAT 1736
Qy 2066 GGGCCGCTTAATCCCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125
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Qy 2126 GGTTCCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185
Dh 1797 GGTTCCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856
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Dh 1857 CAGAGCGTGAAGAGAGAGATTTGATTTCTGCTGTTTACAAAGCCCTGCTGAGAG 1916
Qy 2246 AGTGAATTCAGTGTGAACCTCAGCGCTTACAGCAGACAGCAATACCCGCTACAGCC 2305
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Qy 2366 TGTCCAGCTCCGACAGGATACAGACCCCGACAGCAGCTGTACTACACACCGCTGAGCC 2425
Dh 2037 CGTTCAGCTCCGACAGGATATGACCTTCACAGCAGCTGTACTACACACCGCGAGCC 2096
Qy 2426 GCGCTCCGAGATCTCTGTCAGCCCGCTACCGTGAACAGAGACACCCCTACCTGCAAG 2485
Dh 2097 ACCTCTGAGATCTCTGTCAGCCCGCTTACCTGACCCAGAGCAACCTACCTGTCAGAG 2156
Qy 2486 CCCAGAGAGACAGCAGCTCCCAAGAGAGACTCTCCAGTTCCTGCACTCCAGCTGCA 2545
Dh 2157 TCCCGAAGAGACAGCAGCTTACAGAGAGACTCTCTCCAGTTCCTGCACTCCAGCTGCA 2216
Qy 2546 CTGCTGAGAGCCCGCTGTACGAAGTGAACCTCTCATCTTTGCTGGAAGCACTATGC 2605
Dh 2217 CTGCTGAGAGCCCGCTGTACGAAGTGAACCTCTCTGTTGAGAGAGCACTATGC 2276
Qy 2606 TCTCTTCTCTTGAACCAAAAGCCAGGTGTGTGATCTCTCTTTCTGCTGCTGCT 2665
Dh 2277 TCTCTTCTCTCTGAAACCAAAAGCCAGGTGTGTGATCTCTCTTTCTGCTGCTGCT 2336
Qy 2666 GGGGGTCAAGCTTATGACACCAAGGAGAGAGAGGGGCTGAGCTTACGCAATGT 2725
Dh 2337 GGGGGTCAAGCTTATGAGACACCCGAGTGAAGAGCGGCTGAGCTTACGCAATGT 2396

QY	2726	ATCCGGGAAACCGAGAAATATGACTTTATTTGGTCGACAATTCAAAATCTTTCTTCTCA	2785
Db	2397	TTCCCGGGAAACCGAGAAATATGACTTTATTTGGTCGAGCCAGTTTCAAGTACTTCTTCTCA	2456
QY	2786	CAACATGTATATATGATCACCAGAAAGCAGCTACCCGAATATCCAGAGCTTACTTTACGA	2845
Db	2457	CAACATGTATATATGATCACCAGAAAGCAGCTACCCGAATATCCAGAGCTTACTTTACGA	2516
QY	2846	CTTACACAGAGATTTCAGTAACTGAAGTATGTTCATGTTGGAAACAAAACAGCTTCC	2905
Db	2517	CTTTCATTAAGAGTTCAGCAATGTGAAGTATGTTCATGCTGGAGAGAAACAAAGCACTTCC	2576
QY	2906	CAAAATGTGGCTGCTGACTACTTCTAGAGAGCTTGCTTCAGGAGCTTCAGATGCAATTTGACAG	2965
Db	2577	CAAAATGTGGCTGCTGACTACTTCTAGAGAGCTTGCTTCAGGAGCTTCAGATGCAATTTGACAG	2636
QY	2966	TGACTGGGAAACCGGGAATAATCATGCGCAACATATTCAGAAATGAGATCAGACGATGGAGT	3025
Db	2637	TGACTGGGAAACCGGGAAGATCATGCGCAACATTTATATAAAATGAGATCAGATGACGGGGT	2696
QY	3026	CGTTGCTTACAAACTCCTGGTGCAGAAACCGGACCGCGATTAAGCCATTCGACATCAGCCA	3085
Db	2697	CGTTGCTTACAAACTCCTGGTGCAGAAACCGGACCGCGATTAAGCCATTCGACATCAGCCA	2756
QY	3086	GTTGACTAAACACACGCTTGGTGGATGCAAGTGGCATCTATTAAATCCAGCGCTTTTACAT	3145
Db	2757	GTTGACTAAACACACGCTTGGTGGATGCAAGTGGCATCTATTAAATCCAGCGCTTTTACAT	2816
QY	3146	CTTACTGACGGCTTGGGTGACGAAACGCCGTCGGGTATGTCGTCCTCCAGGCCAACAT	3205
Db	2817	CTTACTGACGGCTTGGGTGACGAAACGCCGTCGTAGCTTACGCTGCCCTCCAGGCCAACAT	2876
QY	3206	CGGGCCACACCGACAGAAATGGGTGCACGACAAAGCCGACTACATGCTCTAAACAAAGGT	3265
Db	2877	CGGGCCCTCACCGGCCGAGGGGTGCATGACAAAGCCGACTACATGCGACAGACGAGCT	2936
QY	3266	GAGAAATCCCGGAGCAGAGACCCATCGAGTATGCCAGTTCCCTTTTACTCAACGGGTT	3325
Db	2937	GAGAAATCCCGAGCAGAGACCCATCGAGTATGCCAGTTCCCTTTTACTCAACGGGCT	2996
QY	3326	GGCGGACACCTCAGACTTTTGTGAGGCAATTGAAAGTAAGAACCATCTGCGAGCAACTA	3385
Db	2997	ACGAGACACCTCAGACTTTTGTGGAACCATAGAAAAATGAGAGTATCTGTAAACAATA	3056
QY	3386	TACGAGCTTGGGGCTGTCCAGTTAACCCAAAGGCTACCCCTTCTCTGAGGAGCAGTA	3445
Db	3057	TACGAGCTTGGGAGCTGTCCAGCTAACCCCAATGGCTACCCCTTCTGTGCGGAGCAATA	3116
QY	3446	CATTGGCCCTCCGCACTGTGCTGTCTGTTCATCAGCGTGTGTGGCTGCGACATTTCT	3505
Db	3117	CATTGACCTCCGCGCACTGTGCTGTCTGTTCATCAGCGTGTGTGGCTGCGACGTTTCT	3176
QY	3506	CGTGTGCGCTGTCTTCTTCTCTGAACCCCTGAGACGGCGCGGATCATTTGATGTGCTGGC	3565
Db	3177	ACTGTGCGCAGTCTTCTCTCTGAACCCCTGAGACGGCGCGGATCATTTGTATGTCTTGGC	3236
QY	3566	CGTGTATGACGGTTCAGCTGTGTGGCATGATGAGGGCTCATGGAATCAAGCTCAGTCCGT	3625
Db	3237	TCTGTATGACCGGTGAGCTTCTTGGCATGATGAGGGCTCATTTGGATCAACGTAAGTCTGT	3296
QY	3626	GGCCCTGGGATCCGATGATGCTTCTGTTGGCATAGGAGTGGAGTTCAACGTTACAGTTGCG	3685
Db	3297	GGCTTGTGATCTCTGATTTGATCTGTGTTGGCATGCGAGTGGAGTTCAACGTTACAGTTGCG	3356
QY	3686	TTTGGCCCTTTCAGACGGCATATCGGGACAAAGAACCGAGGGCTGTGCTTCCCTGGAGACA	3745
Db	3357	TTTGGCCCTTTCAGACGGCATTTGGGGACAAAGAACCGAGGGCTGTGCTTCCCTGGAGACA	3416
QY	3746	CATGTTTGCACCCGCTCTGATGAGCGCGCTGTCCACTGCTTGGGAGTGTGATGCTGGC	3805
Db	3417	CATGTTTCTCCCGCTTTCGAGAGGCTGTGCTGTCCACTGCTGCGGTGTACTGATGCTTCC	3476
QY	3806	GGGATCTAGGTTGCAGCTTCATGTGAGGATTTCTTGTGTGCTGGGCAATCCTCAACAT	3865

[illegible]

Db 4531 TTATTTKKGGAATATTTCTATTAATATTATTAAGGTGACACA - TGTATATATACATGG 4588
Qy 4937 GAAGATGTAAAGTGTATGATGTGGGCTTCTCCACTCTGCCCCAGAGTGTGAGACC 4996
Db 4589 AATATGCTGACAGT -CTATTTCTGGGGCTCTCCACTCTGCCCCAGAGTGTGAGACC 4647
Qy 4997 ACAGTGGGCTCTCCGTTATTTGTGCAATGGGCTCCGTCACACACCAAGCTTATTAAT 5056
Db 4648 ACA--GGGGCCCTTTCCTGCTGTATGATGTGTCTGTGTCACACACCAAGCTTATTAAT 4705
Qy 5057 CTTAAA-----TTTCAGCATATGTGCTGCTGCTTAATATTTATTAATTTACTTGT 5108
Db 4706 TTTTAAAAAATCTCCAGCATATGTGCTGCTGCTTAATATTTATTAATTTACTTGT 4765
Qy 5109 ATATATCTATGCAATATTTGCTATGATGATTAAGATTTATTTGTAAGTTTCTGTTAAA 5168
Db 4766 ATATATCTATGCAATATTTGCTATGATGATTAAGATTA--TTTGTAAAGTTTCTGTTAAA 4824
Qy 5169 ATATTTTAAATTTGCAATATTCACAACTCTGTGATGATGATTAAGTATTAATTTACTTGT 5228
Db 4825 ATATTTTAAATTTGCAATATTCACAACTCTGTGATGATGATTTACTGTTAACTTTTG 4884
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Db 4885 AACACGCTATGCTGATTA-----TTGTTTAAAGACAGACATGAGAAAC 4931

RESULT 8
PCT-US95-13233-3
; Sequence 3, Application PC/TUS9513233
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
; TITLE OF INVENTION: Patched Genes and their use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13233
; FILING DATE: 06-Oct-1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-13233-3

Query Match 71.9%; Score 3801.2; DB 4; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;
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111 1111 111 111 111 1111111111111111 1111 1 11 111

Db 120 CGGGCCCTGGGACAGAGCCGCGCGGAGCGGACAGCGACCGGGGACCGCAGCG 179
Qy 506 TGCTGCGCGCGCGGACCGGACATATCTGACACGGCCACCTACTGGAGCGGCTTCG 585
Db 180 C---GCCGGCGGAGCGGACCTATCTGCACCGGCCACCTACTGGAGCGGCTTCG 236
Qy 566 TCTGAGCAGATTTTCAAGGGGAGAGGCTACTGGCGGAAAGCGCCACTGTGCTGAGAGC 625
Db 237 TCTGAGCAGATTTTCAAGGGGAGAGGCTACTGGCGGAAAGCGCCCTGTGCTGAGAGC 296
Qy 626 GAAGTTTCAAGACTTTTAACTGGGTTTTCATTCAAAAACCTGGGGCAAGTT 685
Db 297 GAAGTTTCAAGACTTTTAACTGGGTTTTCATTCAAAAACCTGGGGCAAGTT 336
Qy 686 CTGGTTGGGCTCTCTATATTTGGGCTTTCGCGGTGGGATTTAAAGCAGCAAGCT 745
Db 357 TTTGGTTGGGCTCTCTATATTTGGGCTTTCGCGGTGGGATTTAAAGCAGCAAGCT 416
Qy 746 CGAGACCAAGCTGAGAGAGCTGTGGTGAAGTTGAGAGCAGATTAAGTGAATTTAA 805
Db 417 CGAGACCAAGCTGAGAGAGCTGTGGTGAAGTTGAGAGCAGATTAAGTGAATTTAA 476
Qy 806 TTATCTGCGCGAAGGATTTGAGAGAGGCTATGTTAATCTCACTCATGATACAGAC 865
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Qy 866 CCTTAAAGAGAGAGTGTCTATATGCTTACACAGAGCGCTCTACACACCTGAGCTC 925
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Qy 1286 TCCAGACTGCGCGCCGACACCGCCCAAAATTTCAACCAAACTCTGATATGGGCTT 1345
Db 957 CCCAGATGCGCTGCGACACCGCCCAAAATTTCAACCAAACTCTGATATGGGCTT 1016
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Qy 1406 GATTTGGGTTGGGACAGTCAAGAACAGCACTGGAATTCGTACGCCCTGCTGCA 1465
Db 1077 GATTTGGGTTGGGACAGTCAAGAACAGCACTGGAATTCGTACGCCCTGCTGCA 1136
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Db 1137 AACCATGTTCCAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1196
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QY 1586 GACATATGTGAGGTGGTTCATCAGAGTGTGACAGACACTCCACTCAAAAGTGTTC 1645
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QY 1706 CGTGGCAGAGGCTACTTACTCATGCTGCGCTATGCTGTCTAACCATGTGCGCTGGGA 1765
DB 1377 AGTGGCAGAGGCTACTTACTCATGCTGCTGTGCTGTATGCTGTGTAACCATGTGCGCTGGGA 1436
QY 1766 CTGCTCAAGTCCAGAGGTGCGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGT 1825
DB 1437 CTGCTCAAGTCCAGAGGTGCGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGT 1496
QY 1826 GGTGAGAGAGCTGGGCTGTGCTCATGTGATGCGAATTCCTTTAAGCGTGCACAACTCA 1885
DB 1497 GGTGAGAGAGCTGGGCTGTGCTCATGTGATGCGAATTCCTTTAAGCGTGCACAACTCA 1556
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DB 1617 ATTCAAGTGAAGAGAGACAAATTAAGAAATCCCTTTGAGAGAGAGACCGGGAGTGCCT 1676
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DB 3297 GCGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3356
QY 3686 TTTGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3745
DB 3357 TTTGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3416
QY 3746 CATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3805

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3417 CATGTTGCTCCGTTGCGAGGCTGCTGTCACCTGCTGGGCTGCTGATGCTTCC 3476
3806 GGGATCTAGTTCGACTTATTTGTCAGGATTTCTTGTGCTGGTGGCATCTCCACAT 3865
3477 AAGGTCGCAATTTGATTTATTTGTCAGATATCTTGTGCTGGCTTGGCCATTTCTCACCGT 3536
3866 CCGGCGCTTCTCAATAGGCTGCTGTTTGGCTTCCCGTGGCTTGTCTTCTTCTTGGAGCAATA 3925
3537 CTGGGGGTTCTCAATAGGCTGCTGCTGCTGCTGCTGCTTCTTCTTCTTGGAGCGTGG 3596
3926 TCCGTAGGTGTCACAGCCCAAGCGCTTGAACCGCTTCCACACCGCTTCCCGTGGAGCGAC 3985
3597 TCCGTAGGTGTCACAGCCCAAGCGCTTGAACCGCTTCCACACCGCTTCCCGTGGAGCGAC 3596
3986 CCGGCGCTTCTCAATAGGCTGCTGTTTGGCTTCCCGTGGCTTGTCTTCTTCTTGGAGCAATA 4045
3657 TCCAGTGTCTCCGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 3716
4046 CGAGTGGAGTATAGTTCCGACGACAGAGTGTGACGCTTCCAGGAGCTTGGGCTTGA 4105
3717 CGAGTGGAGTATAGTTCCGACGACAGAGTGTGACGCTTCCAGGAGCTTGGGCTTGA 3776
4106 CGAGGCGCCACAGAGGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4165
3777 CGAAGCAGACAGAGGCTGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 3836
4166 CCGGCTTGTGCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4225
3837 CCGTGTCTTGTGCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3896
4226 CCGGAGACAGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4285
3897 CCGTGGCGCAACAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 3956
4286 GCGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4345
3957 GCGTGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4016
4346 GCGTGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4405
4017 GCGTGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4076
4406 TCGGGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4465
4077 CCGTGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4136
4466 GCGGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4525
4137 GCGGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4196
4526 GCGGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4581
4197 GCGGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4250
4582 GCGGCGGAGGAGCGCGGAGCGCGCTGCGCCACAGAGTGTGAGAGCGACAGAAAA 4636
4251 TGAAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4310
4637 CCGGCTGAGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4696
4311 CAGGCTGAGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4370
4697 GAGAGGAGGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4756
4371 GAGAGGAGGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4430
4757 AAGAGTGGAGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4816
4431 AAGAGTGGAGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4489
4817 AAGTATGGAGAGGAGGAGTATAGTTCCGACGACAGAGTGTGAGAGCGACAGAAAA 4876

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4490 AATATG-----GGAAGGAGGTTCAATGCTACTGTAAGTATGTA 4530
4877 TATATTTGTAATATTTCTATTAATATTTAAGATGTGACATGTAATATAGAG 4936
4531 TATATTTGTAATATTTCTATTAATATTTAAGATGTGACATGTAATATAGAG 4588
4937 GAAGGATGTAATATTTGTAATATTTGTAATATTTGTAATATTTGTAATATTTGTA 4996
4589 AATATGCTGTAATATTTGTAATATTTGTAATATTTGTAATATTTGTAATATTTGTA 4647
4997 ACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5056
4648 ACA--GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4705
5057 CTAA--TTTACCATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5108
4706 TTTTAAAAAATCTCCAGCATATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4765
5109 ATATTTCTATGCAATATTTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAA 5168
4766 ATATTTCTATGCAATATTTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAA 4824
5169 ATATTTCTATGCAATATTTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAA 5228
4825 ATATTTCTATGCAATATTTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAA 4884
5229 AACAGGCTATGCGTATGTAATTTTGTGTAATAGGAGATATGAGAGGAGGAGGAGGAGG 5280
4885 AACAGGCTATGCGTATGTAATTTTGTGTAATAGGAGATATGAGAGGAGGAGGAGGAGG 4931

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RESULT 9
PCT-US95-13233-9
Sequence 9, Application PC/TUS9513233
GENERAL INFORMATION:
APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
TITLE OF INVENTION: Patched Genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13233
FILING DATE: 06-OCT-1990
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertam I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-13233-9

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Query Match 71.9%; Score 3801.2; DB 4; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;

Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

QY 446 CGGTGCCCGGACGCGCGCTGGAGCGGAGGCGGACGAGCGGGGGCGCTGCCCG 505
 Db 120 CGGGGGCCCTGGGAGGCGCGCGCGCGGAGGCGGAGCGGAGCGGAGCGGAGCG 179
 QY 506 TCCTCGCCCGCGGAGCGGAGCTATCTGCAACCGCCAGCTACTGCGACCGCTTCGC 565
 Db 180 C---GCCCGCGGAGCGGAGCTATCTGCAACCGCCAGCTACTGCGACCGCTTCGC 236
 QY 566 TCTGAGCGATTTCCAAAGGGAGGCTACTGCGCGGAAAGCGCCACTGTGCTGAGAGC 625
 Db 237 TCTGAGCGATTTCCAAAGGGAGGCTACTGCGCGGAAAGCGCCACTGTGCTGAGAGC 296
 QY 626 GAAATTTAGAGACTCTTATTTAACTGGTGTGTACATTCAAAAACCTGCGGCAAGTT 685
 Db 297 GAAATTTAGAGACTCTTATTTAACTGGTGTGTACATTCAAAAACCTGCGGCAAGTT 356
 QY 686 CTGTGTGTGGGCTTCCTCATATTTGGGGCTTTCGCGGTGGGATTTAAAGCGAAGCT 745
 Db 357 TTTGGTGTGGGCTTCCTCATATTTGGGGCTTTCGCGGTGGGATTTAAAGCGAAGCT 416
 QY 746 CGAGACCAACGTGAGAGACTGTGGGTGAGTGTGAGACGAGTAACTGTAATTTAA 805
 Db 417 CGAGACCAACGTGAGAGACTGTGGGTGAGTGTGAGACGAGTAACTGTAATTTAA 476
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 Db 477 TTATATCTGCCAGAGATTGGAAGAGGCTATGTTTAACTCACTCATGATACAGAC 536
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 Db 657 TTTGTGTACAATTCAGAGAGCTTATACAGAAAAGGTTACATGATCAGATATATAGA 716
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 Db 717 ATATCTTACCTTGTGTATATATATACCTTTGAGCTGCTTCGGAAGGCGCCGAAT 776
 QY 1106 ACAGCTTGGGACAGCATACCTCTAGTAAACCTCTTTGGGTTGAGAAATTTGACCC 1165
 Db 777 ACAGCTTGGGACAGCATACCTCTAGTAAACCTCTTTGAGGTTGAGAAATTTGACCC 836
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 QY 1226 GGTGAATTAAGGCTGAGTGTGTCATGTATGATGAGACGCGCCCTCCATATCCGCGGA 1285
 Db 897 GGTGAATTAAGGCTGAGTGTGTCATGTATGATGAGACGCGCCCTCCATATCCGCGGA 956
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 Db 1017 TGTTTGAATGAGTGTATGATGATGATATCCAGAAAATTAATGACAGTGGAGAGATT 1076
 QY 1406 GATTTGGGTGGACAGTCAAGAACAGCACTGGAATAACTGTCAAGCCCAATGCGCTTCA 1465
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 QY 1466 GACCATGTTCCAGTTAATATCTCCCAAGCAATGTACAGACACTTCAAGGGGTACGAGTA 1525
 Db 1137 AACCATGTTCCAGTTAATATCTCCCAAGCAATGTATGAAACACTTCAAGGGGTACGAGTA 1196

QY 1526 TGTCTACACATCAACTGGAACGAGACAAAGCGGACCCATCTGTGAGCGCTGGCAGAG 1585
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 Db 1257 GACTTACGTGAGGTGTTCATCAAAAGTGTGCCCCCAAACTCCACTCAAAAAGTGTCTTC 1316
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 QY 1706 CGTGGCCGCGGCTACTTACTCATCTGCGCTATGCGCTGTCTTACCATGCTGCGGGA 1765
 Db 1377 AGTGGCCGCGGCTACTTACTCATCTGCGCTATGCGCTGTCTTACCATGCTGCGGGA 1436
 QY 1766 CTGCTCCAGTCCCGAGGAGGCGGTGGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCT 1825
 Db 1437 CTGCTCCAGTCCCGAGGAGGCGGTGGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCT 1496
 QY 1826 GGTGACGAGTGGGCTGTGCTCATGTATGATGGAATTTCTTTAAGGCTGCAACAACTCA 1885
 Db 1497 GGTGACGAGTGGGCTGTGCTCATGTATGATGGAATTTCTTTAATGCTGCAACAACTCA 1556
 QY 1886 GGTTTTCCATTTCTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1945
 Db 1557 GGTTTTCCGCTTTCTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1616
 QY 1946 CTTCAGTGAAGACAGACAGATTAAGAAAGTCCCTTTAGAGACAGGAGCGGAGTGCCT 2005
 Db 1617 ATTCAAGTGAAGACAGACAGATTAAGAAAGTCCCTTTAGAGACAGGAGCGGAGTGCCT 1676
 QY 2006 GAAAGCAGACAGAGACAGAGCTGCGCTCTCAGCTCATCAGCAATGTACAGACCTTCTCAT 2065
 Db 1677 CAAGCGCAGGAGAGCGAGCGGCGCTCAGCTCATCAGCAATGTACAGACCTTCTCAT 1736
 QY 2066 GGCCTGCTTATCCCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125
 Db 1737 GGCCTGCTTATCCCTTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
 QY 2126 GGTGTCAATTTTGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185
 Db 1797 GGTATTCATTTTGTCTGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856
 QY 2186 TCGACGAGAGACAGAGAGTGTATTTCTGCTGTTTACAAAGCCCTGCTGACAG 2245
 Db 1857 CAGACGTGAGAGACAGAGAGTGTATTTCTGCTGTTTACAAAGCCCTGCTGACAG 1916
 QY 2246 AGTGAATTCAGAGTGTGAACCTGAGGCTTACAGCAGACAGACAGACATACCCGCTACAGCC 2305
 Db 1917 GGTGATTCAGAGTGTGAACCTGAGGCTTACAGCAGACAGACAGACATACCCGCTACAGCC 1976
 QY 2306 CCGACCTCCCTACAGACAGCCAGCTTTGCCATGAAGACAGATTAACATGACAGTCCAC 2365
 Db 1977 CCGACCCCTACAGACAGCCAGCTTTGCCATGAAGACAGATTAACATGACAGTCCAC 2036
 QY 2366 TGTCCAGCTCCCGAGGAGTGAAGACCCCAAGACAGAGAGTGTATACACACCCGCGAGCC 2425
 Db 2037 CGTTCAGCTCCCGAGGAGTGAAGACCCCAAGACAGAGAGTGTATACACACCCGCGAGCC 2096
 QY 2426 GCGCTCCGAGATCTGTGTGAGGCGCTGACACGCTGACAGACAGACAGTGTATACACACCCGCTGAG 2485
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 QY 2546 CTGCTCGAGCCCGCTGTAGAGAGTGAAGTGTATCTTTTGTGCTGAGAGAGTGTATGCT 2605
 Db 2217 CTGCTCGAGCCCGCTGTAGAGAGTGAAGTGTATCTTTTGTGCTGAGAGAGTGTATGCT 2276

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2726 ACCTCGGGAAACAGAGAAATATGACTTTATGTGTCACAAATTCAAATATCTTTCTTCTA 2785
2397 TCCCGGGGAAACAGAGAAATATGACTTATAGTGTGCCAGTTCAAGTACTTCTCTTCTA 2456
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2457 CAACATGTATATAGTACACCAAGAGAGAGTACCCGAATATCCAGGACTTACTTACGA 2516
2846 CCAACAGAGAGAGTTCGTAGAGTATGTATGTGTTGGGAAAGAAACAAAGCTTCC 2905
2517 CATTATAGAGATTTTCAGCAATGTGAAGTATGTATGTGTTGGGAAAGAAACAAAGCTTCC 2576
2906 CAACATGTGCTGCTGACTTACTTACAGAGTGGCTTCAAGGACTTCAAGATGCTTTGACAG 2965
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2966 TGACTGGGAAACCGGAAATATGACCAACAAATTCAGAGATGAGATGAGAGGAGT 3025
2637 TGACTGGGAAACCGGAGAGTATGACCAACAAATTCAGAGATGAGATGAGAGGAGT 2696
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2757 GTTGTACTAACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2816
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2937 GAGAAATCCCGGAGAGAGGCCCATGAGATGGCCAGTTCCTTCTTACCTCAAGCGGCT 2996
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3117 CATCAGCTGGGCTGCTGCTGCTGTCTTCTATCAGAGCTGTGTGTGTGTGTGTGTGTGTGT 3176
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3237 TCTGTATGAGGCTGAGAGCTTGTGTGGCATGTGTGGGCTTCAAGGAAATGAGTCAAGTGTGTGT 3296
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3297 GCGTGTGCTATCTGTATGAGGCTTGTGTGGCATGTGTGGGCTTCAAGGAAATGAGTCAAGTGTGT 3356
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3417 CATGTTTGTCTCCGTTCTGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3476
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3597 TCCCTGAGGTGTCTCCAGCCACAGCGGCTTGAAGCCGCTGGCCACACCCCTCCCTGAGCCAC 3656
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4046 CGACTGAGATATATTTCCAGACAGAGTGTAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 4105
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4106 CGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4165
3777 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3836
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3897 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3956
4286 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4345
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4346 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4405
4017 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4076
4406 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4465
4077 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4136
4466 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4525
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4526 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4581
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4582 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4636
4251 TGAAGCTACCTGTAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4310
4637 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4696
4311 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4370
4697 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4756
4371 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4430
4757 AAGATTTGAAACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4816


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QY 3518 CTTCTTCTGACCCCTGAGAGCCGGGATCATTTGATGTCCTGGCCGTATGACGGT 3577
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Db 2958 GCTTCCTCTCTCCCTTTGGGGCCGCTTCTGATTCCTGACGCTTCTGGCCCTGCTGGC 3017
QY 3578 CGAGCTGTCGGGATGATGGGCTTCATGCGATCAAGCTCAGTGGCCGTCCTGCTGAT 3637
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 3018 CCAGATCTTTGGGGCCATGACTCTGCTGGCATCAAACTCTGGCCATTCGGCAGTCAT 3077
QY 3638 CCGATGCTCTTGTGGCATGAGAGTTCACCGCTTCAAGTTCAGTTCCTTGGCTTCT 3697
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Db 3078 ACTCATCTTCAGCGTGGGATGATGCTGCTGCTCATGTCGATGTCATGCTGGCTTCAT 3137
QY 3698 GAGGGCCATGGGCGACAAAGCCGAGGCGCTGCTTGGCCCTGGAGACATGTTTGCACC 3757
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 3138 GACATCCGTTGGTGAACGACGCGCGCTGCTGACATGACATGATGCTCCGAGACC 3197
QY 3758 CGTCTGATGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3817
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Db 3198 ACTTGTCCAGGCGATGCTGACCTCCGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 3257
QY 3818 CGACTTCATTTGTCAGTATTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3877
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Db 3258 TGAATTTGTAATCCGCGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3317
QY 3878 CAATGGCTGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3937
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Db 3318 CAACAGCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3377
QY 3938 TCCAGCCAGCGCTGTAAGCCCTGCGCCACACCCCTGCGAGCCACCCCGCAGC 3992
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Db 3378 GCCCGTGGAGCATCCAGACCCCATATCCAGCCCTCTCCGCTGCGCCGCGCAGC 3432

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RESULT 11
US-08-460-900C-42

Sequence 42, Application US/08460900C
Patent No. 6165747

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
APPLICANT: Bunciot, David A.
APPLICANT: Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.

```

; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3897
; US-08-460-900C-42

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Query Match 7.8%; Score 411.8; DB 3; Length 3900;
Best Local Similarity 48.9%; Pred. No. 2,7e-89;
Matches 1730; Conservative 0; Mismatches 1542; Indels 263; Gaps 13;

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QY 537 CGGCCAGCTACTGCGAGCCCGCTTCTGCTGAGCAGATTTCCAAAGGGAAGCTACT 596
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Db 82 CGCACCAGCTGGTGGAGCCGCCAAGTGGCGCTGATCAGATAGATAGAGGCAAGCGCGT 141
QY 597 GCGCGAAGAGCGCACTGCTGGTGGAGGGAAGTTCAGAGACTTTAATTAACCTGGT 656
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 142 GCGAGCCGCGAGCGCATCTATCTGCGATCATGATTTCCAGTCCCACTCGAAGCCCTGGC 201
QY 657 TGTTCATTTCAAAAAAAGTCTGCGCAAGTCTTGTGTTGCGGCCCTCATATTTGGGCGC 716
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 202 AGCTCGTGCAGAAAGCAGCGCGGCAAGTGTCTATTTGTGCTATTCCTGCTGCTGCTGCT 261
QY 717 TTTGCGGTGGATTTAAAGCAGCAGAACCTCGAGACCAAGCTGAGAGCTGTGGTGA 776
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 262 TTTGCGGTGGATTTAAAGCAGCAGAACCTCGAGACCAAGCTGAGAGCTGTGGTGA 836
QY 777 GTTGGAGGAGAGTAAAGTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 836
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 322 GAGGGCGCGGCGCTGAGGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
QY 837 ATGTTTAATCTCACTCATGATTAAGACCCCTTAAGAGAGAGAGTGTATGCTGAC 956
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 382 TCGGCGAGCATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
QY 897 ACAGAGGCGCTCTACACACCTGAGCTGCGGCTGAGGCGCGCTGCTGCTGCTGCTGCT 956
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 442 CCGAGGCGCTGCTGAGGCGCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
QY 957 ATGTACACAGGAGTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 1013
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 502 CTCTACAGACCGAGATGGGGGCTGCGCGCATGTGCAACATGCGGAGCAGCCCTCTTC 561
QY 1014 ACAGAACAGGTTACATGATGATGATTAATTAATTAATTTACCTTTGTTATTAATTA 1073
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 562 GAGGAGCATCTACATGAGAGATCTGCGGACCATCTATTCGCTGATCATCATCAG 621
QY 1074 CTTTGGAGCTGCTTGGGAAGGGGAGGAGATTAACATCTGAGGAGCATCTCTCTCT 1129
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 622 CCGCTGAGCTTTCTGGAAGGAGAGCCAGCTGTGGGCTCGGAAATCAGCGGCTGTATA 681
QY 1130 -----AGTTAAACCTCTTTGGGAGGAGCAAACTTGGCAATTTGGAATTTCTGGAAG 1184
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 682 CCAGGCTCAACCAAGCATCTCTGTGAGCCACACTGAAATCCCGCTCTGTGATGAGTAT 741
QY 1185 TTAAG-----AAATTAATCTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1226
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 742 ATGAAGCAGAGATGCTCGAGGAGGAGGAGATTAATTAATTAATTTGATGAGTGAAG 801
QY 1227 CTGAATTAAGGCTGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1286
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 802 ATGAAGCGTGGCGGCTATTCGAGTGTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 861

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Db	2838	CTGCCCCAACACTATCCACGCGCATTCCTCATCTTCTGGGAGCATAGATGACCCCTGGC	2897
Qy	3458	CCACTGGCTGCTGCTGTTCATCAGCGTGGGTGGCTGCGACATTCCTCGTGTGCGCTGT	3517
Db	2898	CTCTCTACAGCGGCATATGCTCTGGCGCTGGCGTACTGGCGGCGCTGGTGGCTCTCCCT	2957
Qy	3518	CTTCCCTTTCGAACCCCTGAGCGGCGGGATCATTTGATGGTCCCTGGCGGCTGATGACGCT	3577
Db	2958	GGTCTCGCTCTCGCTTTTGGGCGCCCGCTTCCTCGATCCTCAGCGCTTCTGGCGCTGGCTGCG	3017
Qy	3578	CGAGCTGTTGGGCATGATGGGCTCATCGGAATCAAGCTCAGTCCGCTGGCCCGTGTCTAT	3637
Db	3018	CCAGATCTTTGGGGCCCATGCTCTGCTGGGCGATCAAACTCCGGCGATTCGGCGAGTCTAT	3077
Qy	3638	CGTGATCGCTTCTGTTGGGATAGAGAGTGAGAGTCAACGTTCAACGTTCACTTGGCTTGGCCTTCT	3697
Db	3078	ACTCATCTCAGCGTGGGCGTATGCTGTGCTTCATATGCTGTGATATACAGTGGGCTTCAT	3137
Qy	3698	GACGGGCATCGGCGACAGAAGAACCGAGGGCTGTGCTTGGCTTGGCCCTGGAGGCATGTTTGGAC	3757
Db	3138	GACATTCGGTTGGGAACCGAGAGCGCGCGCTTCAGCTGAGATGACAGATGATGTCCTCGGAGAC	3197
Qy	3758	CGTCTCGGATGGCGCGCGTGTCCACTCTGCTGGGAGTCTATGCTGGCGGAGTTGAGTT	3817
Db	3198	ACTGTGCCACGGGATGCTGACCTCCGAGAGGGCGGTTCATGCTCTCCACAGTGGCCCTT	3257
Qy	3818	CGACTTCATTTGACGATTTATTTCTTCTGCTGTGGCGCATCCTGCACATCCCTGGCGGTTCT	3877
Db	3258	TGAGTTTGTGATCCGGCACTTGTGCTGGCTTCTGTCTGTGTGTCTTATGTCGTTGGCGCTG	3317
Qy	3878	CATGGGCTGGTTTTCCTCCGCTGCTTGTGCTTTCCTTTTGGACATATCCTGAGTGTCT	3937
Db	3318	CAACAGCCCTTTTGGTGTTCCTCCCTACCTACAGACATGTTGGGACCGGAGGCGAGCTGT	3377
Qy	3938	TCCAGCGACAGGCTTAAACCGCCTCGCCACACCTCCCTCCCTGAGCGACCCGCCAC	3992
Db	3378	GCTCGCTGGAGATCCAGACCGCATATCCAGCGCCTCTCGGCTGTCCGCTGGCGAC	3432

RESULT 12
US-08-540-406-5
Sequence 5, Application US/08540406
Patent No. 5837538
GENERAL INFORMATION:
APPLICANT: SCOTT, MATTHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249

```

: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4434 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-540-406-5

```

Query Match	7.7%	Score 405;	DB 2;	Length 4434;
Best Local Similarity	48.8%;	Pred. No. 1.2e-87;		
Matches 1711;	Conservative 0;	Mismatches 1550;	Indels 246;	Gaps 13;

QY	537	CGGCGCAGCTACTGCGACCCCGGCTTCGCTCGTGGAGACAGTTTCCAGAGGGGAAAGCTACT	596
Db	283	CGCACCAGCTGGGGTGGACGCCCCCAAGTGGCCCTCGATCGATTAGTTAAGGGCAAAAGCCGT	342
QY	597	GCGCGGAAAAGCCCACTGTGGCTGAGAGCGAGTTTCAGAGACTCTTATTTAAACTGGGT	656
Db	343	GCGCACCAGCGCGCGATCTATCTGGCATCGATTATTCAGTCCCACTCCAGCAAAACCTCGGC	402
QY	657	TGTTTCATTTCAAAAAACACGCGCGCAAGTTCTTGTTGGTGGGCCGTCATATTGGGGCC	716
Db	403	AGCTCCGTCGCAAAAGCAGCCGGGCAAGTCTATTGCGCTATCTCGTGCTGAGCACC	462
QY	717	TTCCGGGTTGGATTAAAAAGCAGCAACTTCGAGACCCAGCTGAGAGACTGTGGTGGAA	776
Db	463	TTCTCGTCGGGCTGGAAGAGCGCCAGATCCACTCCAGAGTGGCAACGAGTGGATCCAG	522
QY	777	GTTGGAGGACGAGTAGTGTGTAATTAATTATCTGCCAGAAAGATTGGAAAGAGCT	836
Db	523	GAGGGCGGGGCTGGAGGCGAACTGGCCCTACACAGAGAAGATCGCGGAGAGCAG	582
QY	837	ATGTTTAATCCCACTCATGTATACAGACCCCTTAAGAAAGAGGTGCTAATGTGCTGCAC	896
Db	583	TGCGGCACGCAATCAGTGTCTCATTCAGAGCAGCCAGCCGGAAGCTCTCGTCTTGAT	642
QY	897	ACAGAGCGGCTCTTACACACCTTGAGCTGGCACTCCAGGCCAGCGGTCCATGTATAC	956
Db	643	CCGCGAGGGGCTCTTCCCACTGGAGGCTCTGGTCAAGCCACCCGCGTCMAAGTGCAC	702
QY	957	ATGTCAACACGAGCAGGAAATTTGAAACATTTGTGTACAAATCAGAGAGC---TATC	1013
Db	703	CTCTACGACACCGAATGGGGGCGCTGCGCAGATGTGCAACATGCCAGACGCGCTCTTTC	762
QY	1014	ACAGAAACAGGTTCATGTGATCAGATATAGAAATATCTTACCTCTTTGATTATTACA	1073
Db	763	GAGGCATCTACTACTACATGAGCAGATCTGCGCACCTCATTTCCGTCTGATCATCAG	822
QY	1074	CCTTTGAGCTGCTTCTGGGAAGGGCGAAATTACAGTCTGGAGACGATACCTCTCT---	1128
Db	823	CCGCTGGAGCTGTTTCTGGGAGGGAAGCCACACTTGGGTCGGGATCAGCGCTGTTATA	882
QY	1130	-----AGGTAAACCTCTTTCGGGTGGACAAACTTGCACCCTTTGAAATTCGTGAAGAG	1184
Db	883	CCAGGCGTCAACCAACGACTCCCTGTGAGCACCCCTGATATCCCGCCTCTGTGATCAGTAT	942
QY	1185	TTAA-----AGAAATTAACATATCACTAGTGACAGCTGGAGGAATG	1228
Db	943	ATGAACAACAAAGATGTCGAGGAAAAAGATACGTTGACTTCGAGACCTGTGACACATAC	1002
QY	1227	CTGAATTAAGGCTGAGGTTGGTATGTTACATGTAGACCGCCCTCCCTCAATCCGCCGAT	1286
Db	1003	ATGAAGCGTGGCCATTGTGGCACTGCTCATGTGAGAGAGCCCTCTGCAACCCACTGAAT	1062
QY	1287	CCAGACTGCGCCCGCACAGACCCCCCAACAAAATTCAACCAAACTCTTGTATATGGCCCTT	1346
Db	1063	CCCAATTGCGCCGAGACAGCGCACCGAACAAGAACAGACCAACGCGCGGATGTGGAGCC	1122
QY	1347	GTTTGAATGCTGATGTATAGCTTATCCAGAAAGTATATGCACTTGGCAGAGAGAGTTG	1406
Db	1123	ATCTGCTCCGGAGGGCTGCTACGGTTATGCGCGCAACCATCTGACATGGCCGAGAGACTG	1182

Qy	1467	ACGATGTCGAGTTATATAGTCGCCAAGCAAAATGTACGAGCTTCGAGGGGATACGAGTAT	1526
Db	1243	TGCGGTGGTGCAGCTATATAGCCGAGAAAGAAATGTACGACCACTGGCAGACAACTACAG	1302
Qy	1527	GTCCTACACATCAACCTGGAACGAGACAACAAGCGGAGCCATCCGTGAGGCGTCGGCAGAG	1586
Db	1303	GTGCACACATCTTGATGTGAGCGCAGGAGAAAGGAGGGAGGTTTGAACGCTGGCAGGCG	1362
Qy	1587	ACATATGTGGAGGTGGTTTCATCAGAGTGTCCACAGAA-----CTCCACTCA	1634
Db	1363	AACCTTTTCGGGGAGGTGGAAACAGCTGCTACGCTAAACATTCGAGAAATTTGCCACAACCTAC	1422
Qy	1635	ANGGTGCTTTCCTTACACACCAAGACCCCTGGACAGACATCTGGAATCTCTCTGTGACGTC	1694
Db	1423	GATATCTACGTGTTCAGCTCCGGCTGCACCTGTGAATGACATCTGGCCAAAGTTCTCCATTCGC	1482
Qy	1695	AGTGTATCCGCGGTGGCCAGCGGCTACTTACTATCTCCGCGCTATGCCCTGTCTAACCATG	1754
Db	1483	ACGCGCTTTCATTTGTCATCTGACGGCGCGTGCACCGCTTTTGTATCCCTTTTGCACGCTC	1542
Qy	1755	CTGCGCT---GGGACGTGCTCAAGTCCCAAGGGGTGGCGGGCTGGCTGGCCGTCGTCG	1811
Db	1543	CTCCGCTGGAGGAGACCCCGTCCGTGGCCACAGACAGTGTGGCCGTGGCCGAGTTCTGTCTC	1602
Qy	1812	GTGTGCACTGTAGTGGCTCAGAGACATGGGCGCTGTGCTCATTTGATGGAATTTCCCTTTAAC	1871
Db	1603	ATGTGCTTCAGTACCCGCGCGGATTTGGGATTTGTACGCCCTCGCTGGTATCTTTTCAAT	1662
Qy	1872	GCTGCACACATCAGGTTTTTGCCATTTTCTGCTCTGTTGTGTGTGTGTGTGTGTGTGTGT	1931
Db	1663	GGCGTACCGCT-----GCTATGGCGAGAGCAATCGCGGGAGCACAACTG	1713
Qy	1932	CTTCTGGCCACCGCTTTCAGATCAACAGACACAATATAAGAAATCCCTTTTGGAGCAGC	1991
Db	1714	ATTCTCAAGAACCCGACAGCAACCCAGGTGGTTCCGTTTTTGGCCCTTGGTGGGGGTC---	1770
Qy	1992	ACCGGGAGTGCCTGAAAGCGCACAGGACCGACGCTGGCCCTCACGTGCATCAGCAATGTC	2051
Db	1771	-----GATCACTACTTTCATATAGTGGGACCGAGCATCTGTTCAAGTGCCTCAGCACCGCA	1824
Qy	2052	ACAGCCCTTTCATGAGCGCGGTTAATCCAAATTTCCGCTCTGGGCGGTTCTCCCTCAG	2111
Db	1825	GGATCTCTTCTTTCGGCGCGCTTATTTCCGGTGCGGCTTTGAAAGATATTCTGTCTCAG	1884
Qy	2112	GCAGCGGTACTAGTGTGTTCAAATTTTGGCATGGTTCGCTCATTTTCTCGCAATTTCTC	2171
Db	1885	GCTGCATCTATATGTGCTCCAAATTTGGCAGCGGCTCTATTGGTTTTTCCGGCCATATTT	1944
Qy	2172	AGCATGGATTTATATGAGCGCAGGAGACAGAGATGATATTTTCTGCTGTATTACAGC	2231
Db	1945	TGCTTTGATATTACGGGAGAGCTACCGCGCGGACGAGGCGGACATCTTCTCTGCTGT---TTT	2001
Qy	2232	CCCTGCGGTGAGCAGAGTGAATTCAGGTTTGAACCTTCAGGCTTACACCGACACACAGCAAT	2291
Db	2002	CCGGTGTGGAAGAAACAGCGGAAAGTGTGCACCTCCGGTGTGCGCTGAACACACACAC	2061
Qy	2292	ACCCGCTACAGCCCCCACCCTCCCTTACAGAGCCACAGCTTTTGCCCATGAAACGAGATT	2351
Db	2062	GGGCGCGGGGCCCGGCATCCGAAGAGCTGCAACACA-----	2098
Qy	2352	ACCATGCAGTCTCACTGTCCAGCTCCGACGAGAGTACGACCCCCACACGACAGTGTACTAC	2411
Db	2099	-----	2098
Qy	2412	ACCACCGCTGAGCGCGCTCCGAGATCTGTGTGACGCCCGTCAACCGTGTACACAGACACC	2471
Db	2099	-----ACAGGGTGCAGCTCCCGCC	2118
Qy	2472	CTGAGCTGCCAGAGCCCGAGAGCAGCAGCTCCACAAGGAGCACTGCTCTCCACTTTCCTC	2531
Db	2119	CAGCATCTCTTCTGTGGAACAGAGGCGAGACATCTCCTTGGAGACAGTCACTGCTGGCGTCC	2178
Qy	2532	GACTCCAGCCTCACTGCTCTGAGCGCCCGCTGTACGAAGTGGACATCTCATCTTTTGTCT	2591

[illegible]

Db 3208 GGCATCAACTCTCGCCATTCGGCATGATCACTCATCTCAGCGCTGGCATGATGCTG 3267
 QY 3666 GAGTTCACCGTTACAGTCTTGTGGCTTTCAGCGCCATCGGCAACAAGACCGCAGG 3725
 Db 3368 TGCTTCAATGTCGTATGATCACTGGGCTTCATGACATTCGCTGGCAACGACGCGCGC 3327
 QY 3726 GCTGTGCTGGCCCTGAGACACATGTTTGACACCGCTGCTGGATGGCGCGCTGTCACACTG 3785
 Db 3328 GTCCAGCTGACATGACATGATGCTCCGAGACCACTTGTCCAGCATGCTGACCTCCGGA 3387
 QY 3786 CTGGAGTGTGATGCTGGCGGATCTGATGCTGACCTCATGCTGACGATTTCTTTCGT 3845
 Db 3388 GTGGCCGGTTCATGCTCTCCACGTCGCCCTTTGATTTGATCGGACCTTCTGCTGG 3447
 QY 3846 GTGCTGGGATCTCCACCATCTCGGCGTTCCTCAATGGGCTGTTTGTGCTCCGCTT 3905
 Db 3448 CTCTGTGTGGTGTCTTATGCTTGGCGCTGCGCAACAGCCTTTTGTGTCCCATCTTA 3507
 QY 3906 TTGCTTCTTGTGGACCATATCGAGGTGTCTCCAGCCAAAGGCTTGACCGCTGCGC 3965
 Db 3508 CTGAGCATGCTGGACCGGAGCGAGCTGGTGGCGCTGGAGCATCAAGACCGCATATCC 3567
 QY 3966 ACACTCTCCCTGAGCCACCCCGCAGC 3992
 Db 3568 ACGCCCTCTCCGCTGCCCGTCCGACG 3594

RESULT 14

PCT-US95-13233-5
 Sequence 5, Application PC/TUS9513233
 GENERAL INFORMATION:
 APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
 TITLE OF INVENTION: Patched Genes and their Use
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehm, Hombach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13233
 FILING DATE: 06-OCT-1990
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Berttram I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: a60190-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4434 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 PCT-US95-13233-5

Query Match 7.7%, Score 405, DB 4, Length 4434;
 Best Local Similarity 48.8%; Pred. No. 1.2e-87;
 Matches 1711; Conservative 0; Mismatches 1550; Indels 246; Gaps 13;

QY 537 CGGCCAGCTCTGCGAGCGCGCTTCTGCTCGAGGAGATTTCCAAAGGGAGGCTACT 596
 || ||||| ||||| | || || ||||| ||||| || || |

Db 283 GGCACAGCTGGTGAGACGCCCAAGTGGCTCGATCAGATAGATAGAGGCAAGCGCGT 342
 QY 597 GCGCGAAGAGCCGACCTGCTGAGAGCAAGTTTCAGAGACCTCTTATTTAACTGGGT 656
 Db 343 GCGAGCGGACAGGGGATCTATCTCGATCAGATTTCCAGTCCCACTCGAAACCTTCGCGC 402
 QY 657 TGTTCATTTCAAAAAAATCGCGCAAGTTCTTGGTTGTGGGCTCTCATATTTGGGGC 716
 Db 403 AGCTCCGTGCAAAAGCAAGCGGGCAAGGTGCTATTTCGGCTATCTGGTGTGACACC 462
 QY 717 TTGCGGTGGGATTAAGAGAGCAACCTCGAAGCAACAGCTGAGAGACCTGGGTGAA 776
 Db 463 TTCTGCTGCGGCTGAAAGAGCGCCCAATCCATCCAAAGGTGACACACTGTGATCCAG 522
 QY 777 GTTGGAGAGCAGTAACTGCTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 836
 Db 523 GAGGGGCGCGGCTGAGGGGCAAGTGGCTGACACAGAGAGATGGCGAGAGACGAG 582
 QY 837 ATGTTTAATCTCAACTCATGATACAGACCCCTTAAGAGAGGTCTAATGTCTTCAGC 896
 Db 583 TCGGCGACCATGACGTCTGATTCAGAGACCCAGCAGACCCGAGACGCTCCGCTTCAT 642
 QY 897 ACAGAGCGCTCTTACACACACTGAGCTCGACCTCCAGGCGACGCTGCTCATGTATAC 956
 Db 643 CCGCAGGCGCTGCTTGGCCACCTGAGAGTCTCGTCAAGGCGCACCGCTCAAGGTGAC 702
 QY 957 ATCTACACAGCAGTGGAAATTTGAACATTTGTTCACAAATCAGAGAGAC--TTATC 1013
 Db 703 CTCTACGACACCAATGAGGGGCTGCGCGACATGTGCAACATGCGACAGCGCTCTTC 762
 QY 1014 ACAGAAACAGGTACATGATGATATATGATATATATATATATATATATATATATAT 1073
 Db 763 GAGGGCATCTACATACATCGAGATCTGCGCACCTCAATCCGCTGCTGATCATCAGC 822
 QY 1074 CCTTTGACTGCTTCTGGGAAAGGGGCAATTAATCACTGAGAGACATACCTCT-- 1129
 Db 823 CCGCTGACTGTTTCTGGAGAGGAGCAAGCTTTGGTCCGGAATCAGGGGTGTTATA 882
 QY 1130 -----AGTAAACCTCTTGGCGGTGAGACAACTTGCACCTTTGGAATTCGTAAGAG 1184
 Db 883 CCAGGCTTCACCAACAGCACTCTGTGGACCACTTAATCCCGCTCTGTGATGACGTAT 942
 QY 1185 TTAA-----AGAAATTAATCAAGTGAAGCTGGAGGAATG 1226
 Db 943 ATGAACAAGATGTCGAGAGAAAGATCAGCTTGAAGACCGTGAGAGCATAC 1002
 QY 1227 CTGAATTAAGCTGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1286
 Db 1003 ATGAAGCTGTGGCCATTTGGCTGATGATGATGATGATGATGATGATGATGATGAT 1062
 QY 1287 CCAGACTGCGCGCCAGAGCCCGCAAGAAATTAACCAACCTCTTGAATGAGCTT 1346
 Db 1063 CCAATTCCTCGGACACGACCGACCAAGAACAGACCAACCGCCGCGATGAGAGCC 1122
 QY 1347 GTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
 Db 1123 ATCTGTCCGAGGCTGTACGCTTATGCGGGAAGCAATCATCATGCTGCGGAGAGCTG 1182
 QY 1407 ATGAGGCTGACAGATGAAGAACAGCACTGGAATTAATGATGATGATGATGATGATGAT 1466
 Db 1183 ATTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1242
 QY 1467 ACCATGTTCCAGTAAATGATCTCCCAAGCAATGTCGAGACCTTCAAGGGGTACAGAT 1526
 Db 1243 TCGGTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302
 QY 1527 GTCTCACACATCAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1586
 Db 1303 GTGACCATCTTGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1362
 QY 1587 ACATATGTGAGAGGTCTTCAAGATCAAGAGTGCACAGAA-----CTCACATCAA 1634
 Db 1363 AACTTTTCGGGGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1422

QY	1635	AAGTGGCTTTCTTCTTACACACACGACCCCTGGAGACGATCCGGAATCCCTTCTGAGCTC	1694
Db	1423	GATATCTACAGGTTTACGTTCCGCTGCTACCTGGATGATCTCTGGCCAAAGTTCTCCATCCC	1482
QY	1695	AGTGTCACTCCGCGTGGGACAGGAGGCTACTTACTCATGCTGCGCTATGCGCTGTCTAACATG	1754
Db	1483	AGCGCTGTGTCCATTTGTCTATGGCGGTGGCCGCTCAACGTTTGTATGCTTTTGGACGCTC	1542
QY	1755	CTGCGCT---GGAGCTGCTCCAACTCCCAAGGTGCCGTGGGGCTGGGCTGGCTGGCTG	1811
Db	1543	CTCCCGCTGGAGGACCCCGTCCGTGGCCAGACAGTGTGGGGGTGGCCGGAATTTGCTC	1602
QY	1812	GTTGCACTGTGAGTGGCTGACAGACTGGGAGCCCTGCTCATGTATGATGAGAAATTTCTTAAAC	1871
Db	1603	ATGTGCTTTCAGTACCGCCCGCGGATTTGGGANTTTGCAGCGCTGTGCGGATATGTTTCAAT	1662
QY	1872	GCTGCACAACTCAGGTTTGTGCCATTTCTCGCTCTTGGTGTGGTGTGATATGTTT	1931
Db	1663	GGCTGACCGCT-----GCTATGCGGAGACGAATCGGCGGGAGGCGAACGAAGCTG	1713
QY	1932	CTTTTGCGCCAGCGCTTCAGTGAAACAGACAGAAATAAAGAAATCCCTTTGAGACAG	1991
Db	1714	ATTCTCMAAGACGCGACGACCCAGGTGTGTTCCGTTTGTGGCCCTTGCTGTGGGCGTC---	1770
QY	1992	ACCGGGAGTGGCTGTAAAGCGACAGGAGGACAGTGGCCCTCAGCTGCATCAGCAATGTC	2051
Db	1771	-----GATCACAATCTTCATATAGTGGGACGACAGCATCTGTGATGCTCCGACACACGGA	1824
QY	2052	ACAGCCTTCTTCATGGCCCGCGTTAAATCCCAATCCCGCTGTGGGCGTTCCTCCCTCGAG	2111
Db	1825	GGATCTCTTTTGGCGCCGCTTATTCGGGTGCCGCTTTGAAGTATTTGCTGTGCGAG	1884
QY	2112	GCAGCGGTAGTAGTGGTGTTCAAATTTTGGCATAGTTCTGCTCAATTTTTCCTGCATTTCTC	2171
Db	1885	GCTGCCATGCTATGTGCTCCATTTTGGACGCGGCTCTATATGTTTTCGGCCATGAT	1944
QY	2172	AGCATGATTTATATGACGCGCAGAGGACAGAGATGATTTTCTGCTGTTTACAGC	2231
Db	1945	TCTGTTGATCTACGAGACCTACCGCGCGAGGCGCGACATCTTCTGCTCTGT---TTT	2001
QY	2232	CCCTGGCTGACGAGTAGTTCAGTTGTAACCTTCAGGCGCTTACACGACACACAGCAAT	2291
Db	2002	CCGGTGTGGAAAGAACGCGGAAAGTGTGCACCTCCGGTGTGCGCTGGAACACACACAC	2061
QY	2292	ACCGGCTACAGCCCCCACTCCCTCCCTACAGCAGCCACAGCTTTGGCCATGAAAGCAGATT	2351
Db	2062	GGGGGCGGCGCGGCACTCCGAAGAGCTGTGAACACG-----	2098
QY	2352	ACCATGCAATCTCATCTCCAGCTCCGACGGAGTACACCCGACACGCACTGTACTAC	2411
Db	2099	-----	2098
QY	2412	ACCACGCTGAGCGCGCTCGAGATCTGTGTGACGCCCTGACCCGTGACACAGGAACG	2471
Db	2099	-----ACAGGGTCCGCTCCGCGC	2118
QY	2472	CTCAGCTGCGACAGCCCGACAGACACGACGCTCCCAAGGGACGCTGCTCCCATTTTCC	2531
Db	2119	CAGATCTCTGTGTGGAACAGAGGGCAGACATCTCCCTGGAGCAATCACTACTGTGGCGTCC	2178
QY	2532	GACTCCAGACCTCCACTGCTTCGAGCCCGCTGTACGAAGTGGACATCTCATTTTGT	2591
Db	2179	TTTCTC-----CTTGGCAACTTGTGCT	2199
QY	2592	GAGAGCACTATGCTCTTTCTTCTTGAACCAAAAGCAAGTATGATGATCTTCTT	2651
Db	2200	TTTTCAGCACTACACTCCCTTCTCATGTGGCAGCTGGGGTGAATCTTGACCTGATATGGCT	2259
QY	2652	TTTTGGGCTTTGTGGGGGTAGGCTTATATGGACACACCCAGTAGAGACGGGCTGGAC	2711
Db	2260	TTCTGTGGGCGCTCATATCTCAGCTTGTATGCTCTCAAGCGGCTTCAAGATATGGGCTGGAC	2319

[illegible]

Db 3388 GTGGCCGTGTTCACTGCTCTCCAGCTGCCCCCTTGAAGTTGGATCCGCACTTCTGCTGG 3447
 QY 3846 GTGCTGGCCGATCCCTACACCATCTCGCCGTTCTCAATGGGCTGGTTTCTTCCTCCGCTGCTT 3905
 Db 3448 CTCTGTGTGTGCTTATGCTGGGGCCGCAACAGACCTTTTGTGTTCCCAATCCTA 3507
 QY 3906 TTGTCTTTCTTTGGACCATATCTGAGGTGTCTCCAGCCAAAGGCTTGACCCGCTGCCC 3965
 Db 3508 CTGAGCATGTGGACCGGAGGCGAGCTGTGCCCTGAGCATCCAGACCGCATATCC 3567
 QY 3966 ACACCTCCCTGAGCCACCCCCAGC 3992
 Db 3568 AGCCCTCTCCGCTGCCCGTGGCAGC 3594

RESULT 15 US-08-540-406-7

; Sequence 7, Application US/08540406
 ; Patent No. 5837538
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,406
 ; FILING DATE: 06-OCT-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertiam I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 345 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-540-406-7

Query Match 1.5%; Score 77; DB 2; Length 345;
 Best Local Similarity 51.2%; Pred. No. 1.9e-09;
 Matches 176; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 753 AACGTGAGAGAGCTGGGTGCAAGTTGAGAGACGAGTAAGTCGTGAATTAATTATACT 812
 Db 1 AAGGTCCATACACTTGTGATACAGGAAGGTGTTGCTGAGCATGAGTAGCCTACACG 60
 QY 813 CGCCAGAGATGAGAGAGAGCTATGTTAATCTCACTCATGATGATACAGACCCCTAAA 872
 Db 61 CAGAAATGCTGCGGAGAGATGAGATCTCCACGACAGCTGTAATCCAAACNCCCAA 120
 QY 873 GAAGAGGTGCTAATGTCCTGACCAAGAGCGCTCTACAAACCTGAGCTGGCAGCTC 932
 Db 873 GAAGAGGTGCTAATGTCCTGACCAAGAGCGCTCTACAAACCTGAGCTGGCAGCTC 932

Db 121 GATATGAGGCGCTCGATACTGACACCGGACCGGCTACTGAGGACCTGAGCTGTGAG 180
 QY 933 CAGGCCAGCCGCTGTCATGATATACATGTACAAACAGGACGATGGAATTTGCTGT 992
 Db 181 AAAGCGATCTCGGTGACGGTGACATGTACAGACATCACGTGAGAGNCTCAAGAGACATGTC 240
 QY 993 TACAATCAGAGAGAGCTTATCACAGAAACAGTGTACATGATGATGATATATATCTT 1052
 Db 241 TACTGCCAGCATATACCGAGNCTTCGATACGCACTTTATCGAGCAGATCTTGAGAGATC 300
 QY 1053 TACCTTGTGTTGATTAATTAACACCTTTGAGACTGCTTCTGGAAGG 1096
 Db 301 ATACCGTGGCGATCATACAGCCGCTGAGATTGCTTTGGAGG 344

Search completed: January 13, 2001, 09:20:03
 Job time: 11106 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:53:33 ; Search time 4849.57 Seconds

(without alignments)
3868.488 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288

Sequence: 1 GAATTCGGGGGACCGCAAGG.....TATGAGAAAGCCCGGGAATT 5288

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 12197726 seqs, 1773875003 residues

Total number of hits satisfying chosen parameters: 24395452

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5288	100.0	5288	13	US-08-954-655-18
2	5288	100.0	5288	13	US-08-954-668-18
3	5288	100.0	5288	13	US-08-954-701A-18
4	4684.8	88.6	6568	12	US-08-857-636-1
5	3801.2	71.9	5187	13	US-08-954-655-3
6	3801.2	71.9	5187	13	US-08-954-655-9
7	3801.2	71.9	5187	13	US-08-954-668-3
8	3801.2	71.9	5187	13	US-08-954-668-9
9	3801.2	71.9	5187	13	US-08-954-701A-3
10	3801.2	71.9	5187	13	US-08-954-701A-9
11	1176.4	22.2	4030	14	US-09-060-930A-1
12	1176.4	22.2	4030	14	US-09-293-93A-1
13	1173.2	22.2	4391	16	US-09-207-857-1
14	593.8	11.2	2082	14	US-09-060-939A-9
15	593.8	11.2	2082	16	US-09-293-505-9
16	472.2	8.9	1734	12	US-08-857-636-58
17	450.2	8.5	3861	42	US-60-171-625-89
18	450.2	8.5	3861	42	US-60-173-464-3397
19	450.2	8.5	3861	44	US-60-191-637-4082
20	450.2	8.5	3861	44	US-60-191-681-3260
21	450.2	8.5	3861	46	US-60-219-005-44
22	449	8.5	485	16	US-09-235-076-21578
23	449	8.5	485	16	US-09-289-768-26469
24	449	8.5	485	17	US-09-332-782-21578
25	433.8	8.2	2032	14	US-09-082-267A-1
26	433.8	8.2	2032	14	US-09-082-267A-1
27	427.2	8.1	445	14	US-09-036-521A-1124
28	427.2	7.9	3901	41	US-60-167-216-110
29	411.8	7.8	3900	8	US-08-462-388D-42
30	411.8	7.8	3900	10	US-08-674-509B-42
31	411.8	7.8	3900	13	US-08-954-128-42
32	411.8	7.8	3900	13	US-08-954-658-42
33	411.8	7.8	3900	13	US-08-954-740-42
34	411.8	7.8	3900	13	US-08-954-771-42
35	411.8	7.8	3900	13	US-08-957-874-42
36	411.8	7.8	3900	22	US-09-639-655-42
37	411.8	7.8	3900	24	US-09-711-724-42
38	411.8	7.8	3900	55	US-09-736-476-42
39	411.8	7.8	3900	55	US-08-319-745-5
40	405	7.7	4434	13	US-08-954-655-5
41	405	7.7	4434	13	US-08-954-668-5
42	405	7.7	4434	13	US-08-954-701A-5
43	390.4	7.4	482	16	US-09-287-618-5277
44	388.8	7.4	1496	1	PCT-0500-25479-116
45	388.8	7.4	1496	1	PCT-0500-25479-116

ALIGNMENTS

RESULT 1
US-08-954-655-18
Sequence 18, Application US/08954655
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
GOODRICH, LISA V
JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Elliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,655
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36709
REFERENCE/DOCKET NUMBER: SUV-003.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 5288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-954-655-18

Query Match 100.0%; Score 5288; DB 13; Length 5288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGAGCGAAGAGTGGCGGAGCGCGGCGCGGAGAGAGCTCGGGA 120
DB 1 GAATTCGGGGAGCGAAGAGTGGCGGAGCGCGGCGCGGAGAGAGCTCGGGA 60
QY 61 GCGGCGTTCGCTTCCGCGCAACTGATGTGGCGAGCGCGCGCGGAGAGAGCTCGGGA 120
DB 61 GCGGCGTTCGCTTCCGCGCAACTGATGTGGCGAGCGCGCGCGGAGAGAGCTCGGGA 120
QY 121 CCCCCGCAATGTGCAATGGAAGCGCAGAGGCTGTGACTCCCGGAGCGCGCGGCG 180
DB 121 CCCCCGCAATGTGCAATGGAAGCGCAGAGGCTGTGACTCCCGGAGCGCGCGGCG 180
QY 181 GCAGGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GCAGGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 CGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
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DB 301 GAGCGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 361 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

DB 361 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
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DB 421 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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DB 481 GCAGGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 541 CCAGCTACTCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
DB 541 CCAGCTACTCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 601 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
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DB 661 ACATTCGCAAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 CCGTGGGATTTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 CCGTGGGATTTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 GAGGACGAGTAAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
DB 781 GAGGACGAGTAAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 TTAATCTCAATCATATATATATATATATATATATATATATATATATATATAT 900
DB 841 TTAATCTCAATCATATATATATATATATATATATATATATATATATATATAT 900
QY 901 AAGGCTCTCAACACACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
DB 901 AAGGCTCTCAACACACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 961 ACAACAGCAGTGAATTTGGAACATTTGTTTACAAATCAGAGAGCTTATACAGAA 1020
DB 961 ACAACAGCAGTGAATTTGGAACATTTGTTTACAAATCAGAGAGCTTATACAGAA 1020
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DB 1021 CAGGTTACATGATCAGATATATATATATATATATATATATATATATATATAT 1080
QY 1081 ACTGCTTCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 ACTGCTTCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 CTTTGGCGGTGCAAACTTTCGACCTTTTGAATTCCTGGAAGAGTTAAAGAAATTA 1200
DB 1141 CTTTGGCGGTGCAAACTTTCGACCTTTTGAATTCCTGGAAGAGTTAAAGAAATTA 1200
QY 1201 ATCAAGTGAACAGCTGGGAGGAAATGCTGTAATTAAGGCTGAGTGTGATGTT 1260
DB 1201 ATCAAGTGAACAGCTGGGAGGAAATGCTGTAATTAAGGCTGAGTGTGATGTT 1260
QY 1261 ACCGCGCTGCTGCAATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB 1261 ACCGCGCTGCTGCAATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1321 CAACCAAACTCTTGATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
DB 1321 CAACCAAACTCTTGATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1381 AGTATATGCACTGGCAGAGAGAGTTGATTTGATTTGATTTGATTTGATTTG 1440
DB 1381 AGTATATGCACTGGCAGAGAGAGTTGATTTGATTTGATTTGATTTGATTTG 1440
QY 1441 AACTGTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
DB 1441 AACTGTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500

OY	1501	ACGAGCACTTCAAGGGGTACGAGTATGTCACACATCACTCACTGGAACGAGGACAAAGCG	1560
Db	1501	ACGAGCACTTCAAGGGGTACGAGTATGTCACACATCACTGGAACGAGGACAAAGCG	1560
OY	1561	CACCACTTCTGGAGGCGCTGGCAGAGGACATATGTGGAGTGGTTCATCAGAGTCTGGAC	1620
Db	1561	CACCACTTCTGGAGGCGCTGGCAGAGGACATATGTGGAGTGGTTCATCAGAGTCTGGAC	1620
OY	1621	AGAACTCCACTCAAAAGGTCTTTCCTTACCAACCAACGAGCCCTGGAGACATCTGAAAT	1680
Db	1621	AGAACTCCACTCAAAAGGTCTTTCCTTACCAACCAACGAGCCCTGGAGACATCTGAAAT	1680
OY	1681	CCCTTCTGACGTCAGTGTATCCGGGTGGCCAGCGGCTCACTATCATGTGGCCATG	1740
Db	1681	CCCTTCTGACGTCAGTGTATCCGGGTGGCCAGCGGCTCACTATCATGTGGCCATG	1740
OY	1741	CCGTCTAACCATGCTGCGCTGGAGCTGCTCCAAAGTCCAGAGGCGCGTGGGCTGGCTG	1800
Db	1741	CCGTCTAACCATGCTGCGCTGGAGCTGCTCCAAAGTCCAGAGGCGCGTGGGCTGGCTG	1800
OY	1801	GCGTCTGCTGGTTCGACACTGTCAGTGGCTGACAGACTGGGCTGTGCTCATTTGACGAA	1860
Db	1801	GCGTCTGCTGGTTCGACACTGTCAGTGGCTGACAGACTGGGCTGTGCTCATTTGACGAA	1860
OY	1861	TTTTCTTTAAACGCTGCAACAACTCAGATTTTGGCATTTCCGCTTGGGTGGTGGTGG	1920
Db	1861	TTTTCTTTAAACGCTGCAACAACTCAGATTTTGGCATTTTCGCTTGGGTGGTGGTGG	1920
OY	1921	ATGATGTTTTTCTTGTGGCCCAACGCTTCACTAGTAAGACAGACAGATAAAGATCCCTT	1980
Db	1921	ATGATGTTTTTCTTGTGGCCCAACGCTTCACTAGTAAGACAGACAGATAAAGATCCCTT	1980
OY	1981	TTGAGAGACAGGACCGGGGAGTGGCTAAAGGCAACAGAGCAGCGTGGCCCTCAGCTCCA	2040
Db	1981	TTGAGAGACAGGACCGGGGAGTGGCTAAAGGCAACAGAGCAGCGTGGCCCTCAGCTCCA	2040
OY	2041	TCAGCAATGTCAACAGCCTTCTTCATGAGCGCGCTTAATCCCAATTCGCTGTGGGCGCT	2100
Db	2041	TCAGCAATGTCAACAGCCTTCTTCATGAGCGCGCTTAATCCCAATTCGCTGTGGGCGCT	2100
OY	2101	TCTCCCTCCAGGACGGGTAATGTAAGTGTGTTCAATTTTGGCATGTTCTGCTCATTTTTC	2160
Db	2101	TCTCCCTCCAGGACGGGTAATGTAAGTGTGTTCAATTTTGGCATGTTCTGCTCATTTTTC	2160
OY	2161	CTGCAATTCACAGCATGAGATTTATATCGAGCGGAGGACAGACAGTGGATATTTTTCGCT	2220
Db	2161	CTGCAATTCACAGCATGAGATTTATATCGAGCGGAGGACAGACAGTGGATATTTTTCGCT	2220
OY	2221	GTTTTTACAAGCCCTTGCTGTCAGAGAGTATTTAGTTGTAACCTCAGGCTTACACGCACA	2280
Db	2221	GTTTTTACAAGCCCTTGCTGTCAGAGAGTATTTAGTTGTAACCTCAGGCTTACACGCACA	2280
OY	2281	CACAGGACATATACCCGCTACAGCGCCCCCACTCTCCTAACGACGCACACAGTTTGGCCATG	2340
Db	2281	CACAGGACATATACCCGCTACAGCGCCCCCACTCTCCTAACGACGCACACAGTTTGGCCATG	2340
OY	2341	AAACGCAGATTTACATGACAGTCCACATGTCCGACAGGAGTACGAGTGGAGTGGAGTGGAGT	2400
Db	2341	AAACGCAGATTTACATGACAGTCCACATGTCCGACAGGAGTACGAGTGGAGTGGAGTGGAGT	2400
OY	2401	ACGTGTACTACACACACCGCTGAGCCGCGCTCCGAGATCTCTGTGACAGCCGCTACACGCTGA	2460
Db	2401	ACGTGTACTACACACACCGCTGAGCCGCGCTCCGAGATCTCTGTGACAGCCGCTACACGCTGA	2460
OY	2461	CACAGGACACCCCTACGCTGCGAGAGCCCAAGAGACACAGCTCCACAAGGAGACTGTCT	2520
Db	2461	CACAGGACACCCCTACGCTGCGAGAGCCCAAGAGACACAGCTCCACAAGGAGACTGTCT	2520
OY	2521	CCCACTTCTCCAGCTCACACTCTCCATGTGCTCGAGCCGCCCTGTACGAAAGTGGACACTCT	2580
Db	2521	CCCACTTCTCCAGCTCACACTCTCCATGTGCTCGAGCCGCCCTGTACGAAAGTGGACACTCT	2580

OY	2581	CAGCTTTGCTGGAGAGCACTAAGTCCTTCCCTTGAACCAAAAGCCAGGTAATGG	2640
Db	2581	CATCTTTTGCTGAGAGCACTAAGTCCTTCCCTTGAACCAAAAGCCAGGTAATGG	2640
OY	2641	TGATCTTCCTTTTTCGGGCTTCTGGGGGTGACGCTTTATMGCCACCACCCGATGAGAG	2700
Db	2641	TGATCTTCCTTTTTCGGGGTCTGGGGGTGACGCCCTTATMGCCACCACCCGATGAGAG	2700
OY	2701	ACGGGCTGACCTTACGGGACATTGTACTCTGGGAAACAGAGATATGACTTTATTTGCTG	2760
Db	2701	ACGGGCTGACCTTACGGGACATTGTACTCTGGGAAACAGAGATATGACTTTATTTGCTG	2760
OY	2761	CACAAATTCAAATCTTTTCTTCTTACAAACATGATATAGTACCCACAAAGCAGACTACC	2820
Db	2761	CACAAATTCAAATCTTTTCTTCTTACAAACATGATATAGTACCCACAAAGCAGACTACC	2820
OY	2821	CGAATATCCAGCACTTACTTTACGACCTACACAGGATTTTCAGTAAGTGAATGTGCA	2880
Db	2821	CGAATATCCAGCACTTACTTTACGACCTACACAGGATTTTCAGTAAGTGAATGTGCA	2880
OY	2881	TGTTGGAAACAAACAAAGCTTCCCAAAATGTGGGTGCACTACTTTCAGAGACTGGCTTC	2940
Db	2881	TGTTGGAAACAAACAAAGCTTCCCAAAATGTGGGTGCACTACTTTCAGAGACTGGCTTC	2940
OY	2941	AGGGACTTGAGATGCAATTTGACAGTGTACTGGGAAACCGGGAAATCATGCAAAACATY	3000
Db	2941	AGGGACTTGAGATGCAATTTGACAGTGTACTGGGAAACCGGGAAATCATGCAAAACATY	3000
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Db	3001	ACAGAGATGGATCAGACGATGGAGTGCCTTCCCTACAAACTCTGTGTGTCAAACCGGACCC	3060
OY	3061	GGGATTAAGCCATCGACATCAGCAGAGTTCGCTAAACAGCTCTGTGTGATGACAGATGCA	3120
Db	3061	GGGATTAAGCCATCGACATCAGCAGAGTTCGCTAAACAGCTCTGTGTGATGACAGATGCA	3120
OY	3121	TCATTAATCCGACGGCTTCTTCTACTACTGACGGCTTGGGTGACGACGACCCGCTGC	3180
Db	3121	TCATTAATCCGACGGCTTCTTCTACTACTGACGGCTTGGGTGACGACGACCCGCTGC	3180
OY	3181	CGTATGCTGCTCCACGAGCAACATCCGGCCACACGACAGAGATGGGTCCACAGACAAG	3240
Db	3181	CGTATGCTGCTCCACGAGCAACATCCGGCCACACGACAGAGATGGGTCCACAGACAAG	3240
OY	3241	CCGACTACATGCTCTGAACAGGCTGAGAATCCCGGACAGAGACCCCATCGAGTATGCC	3300
Db	3241	CCGACTACATGCTCTGAACAGGCTGAGAATCCCGGACAGAGACCCCATCGAGTATGCC	3300
OY	3301	AGTTCCTTTTACGTCACAGGGGTTCGGGACACGCTCAGACTTGTGTGAGGCAATTGAAA	3360
Db	3301	AGTTCCTTTTCTTACCTCAAGGGGTTCGGGACACGCTCAGACTTGTGTGAGGCAATTGAAA	3360
OY	3361	AAATTAAGGACCATCTGACACCAACTATAGCAGCCTGGGGGCTGTCAGTTACCCCAACGCT	3420
Db	3361	AAATTAAGGACCATCTGACACCAACTATAGCAGCCTGGGGGCTGTCAGTTACCCCAACGCT	3420
OY	3421	ACCCCTTCCTCTTCTGGGAGGAGTACATGGGCTCCGCCACTGTGCTGCTGTATGCA	3480
Db	3421	ACCCCTTCCTCTTCTGGGAGGAGTACATGGGCTCCGCCACTGTGCTGCTGTGTATGCA	3480
OY	3481	GGGTGTGTGGCTGACATATTCCTGTGTGGCTGTCTTCTTCTTGTGAACCCCTTGACGG	3540
Db	3481	GGGTGTGTGGCTGACATATTCCTGTGTGGCTGTCTTCTTCTTGTGAACCCCTTGACGG	3540
OY	3541	CCGGGATATTTGTATGCTCTTGCGGCTGATGACGGTTCGACAGCTGTTCCGGCATATGGCC	3600
Db	3541	CCGGGATATATTTGTATGCTCTTGCGGCTGATGACGGTTCGACAGCTGTTCCGGCATATGGCC	3600
OY	3601	TCATGGGATCAAGGTCAGTGGCGGCGCCGTGGTCAATCCGATGCGTCTGTTGGCATAG	3660
Db	3601	TCATGGGATCAAGGTCAGTGGCGGCGCCGTGGTCAATCCGATGCGTCTGTTGGCATAG	3660
OY	3661	GAGTGAAGTTCACGGTTCACGTTGCTTGGCTTTCTTGACGGCCATCGGCGACAAACACC	3720

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Db 3661 GAGTGGAGTTACCGTGTACGTTGGCTTTCTGACGGCCATCGGCGAACAAGACC 3720
Qy 3721 GCAGGGCTGTCTTGGCTTGGAGCAGCATGTTTGCACCCGCTCTGATGGCCGCTTCCA 3780
Db 3721 GCAGGGCTGTCTTGGCTTGGAGCAGCATGTTTGCACCCGCTCTGATGGCCGCTTCCA 3780
Qy 3781 CTCTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTTCAATTTGACAGTATTTCT 3840
Db 3781 CTCTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTTCAATTTGACAGTATTTCT 3840
Qy 3841 TTGCTGTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTTCAATTTGACAGTATTTCT 3900
Db 3841 TTGCTGTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTTCAATTTGACAGTATTTCT 3900
Qy 3901 TGTCTTTGCTTTCTTTTGGAGCATATTCCTGAGAGTGTCTGACCAACGAGCTTGAACCGCC 3960
Db 3901 TGTCTTTGCTTTCTTTTGGAGCATATTCCTGAGAGTGTCTGACCAACGAGCTTGAACCGCC 3960
Qy 3961 TGCCACACCCCTCCCTGAGCCACCCCGAGGCTGGCTTGGCATGCGCCGCGCC 4020
Db 3961 TGCCACACCCCTCCCTGAGCCACCCCGAGGCTGGCTTGGCATGCGCCGCGCC 4020
Qy 4021 ACACGACAGCGGGGTCTGATTCCTCCGACTCGAGTATAGTTCCAGACAGTGTCA 4080
Db 4021 ACACGACAGCGGGGTCTGATTCCTCCGACTCGAGTATAGTTCCAGACAGTGTCA 4080
Qy 4081 GCTTCAGAGAGAGTGTGGGCACTACGAGAGCCAGAGGGCCGGAGAGCCCTGCCACC 4140
Db 4081 GCTTCAGAGAGAGTGTGGGCACTACGAGAGCCAGAGGGCCGGAGAGCCCTGCCACC 4140
Qy 4141 AAGTATGTGTGAAGACACAGAAAACCCCTTGGCCACTGCTGATGTGTCTATCCG 4200
Db 4141 AAGTATGTGTGAAGACACAGAAAACCCCTTGGCCACTGCTGATGTGTCTATCCG 4200
Qy 4201 AATCCAGGATCACCACCTTGAACCCGAGACAGAGCCACCTGAGATCGAGGTCCC 4260
Db 4201 AATCCAGGATCACCACCTTGAACCCGAGAGAGAGCCACCTGAGATCGAGGTCCC 4260
Qy 4261 TGCCCTCCGGAGGAGGAGCCAGAGCCCGGAGGAGCCCGGAGAGAGGCTTGGG 4320
Db 4261 TGCCCTCCGGAGGAGGAGCCAGAGCCCGGAGGAGCCCGGAGAGAGGCTTGGG 4320
Qy 4321 CACCCCTCTACAGACCGGCGAGAGAGCTTTTGAATTTCTACTGAAGGCAATTCGGCC 4380
Db 4321 CACCCCTCTACAGACCGGCGAGAGAGCTTTTGAATTTCTACTGAAGGCAATTCGGCC 4380
Qy 4381 CTAGCAATAGGGCCGCTGGGGCCCTCGGGGGCCCTGCTCAACACCTCGGAACCCAG 4440
Db 4381 CTAGCAATAGGGCCGCTGGGGCCCTCGGGGGCCCTGCTCAACACCTCGGAACCCAG 4440
Qy 4441 GTCACAGTGCATAGGGAGCTCGTGGCCGGGCTAGTGCAGGCCATCACACGTGACG 4500
Db 4441 GTCACAGTGCATAGGGAGCTCGTGGCCGGGCTAGTGCAGGCCATCACACGTGACG 4500
Qy 4501 CTTCGCTCCGTGATGTGCGCTGACACCGCCGCTTCTCCCTGGGCTTGGGAGAAC 4560
Db 4501 CTTCGCTCCGTGATGTGCGCTGACACCGCCGCTTCTCCCTGGGCTTGGGAGAAC 4560
Qy 4561 CCGGAGGGGAGCTGTGCCAGGCTACCTGAGACATGACACGCGCTTGAAGACCCCC 4620
Db 4561 CCGGAGGGGAGCTGTGCCAGGCTACCTGAGACATGACACGCGCTTGAAGACCCCC 4620
Qy 4621 ACGTCCCTTTCCAGTCCGCTGTGAGAGAGGAGGATTCGAAGGTGGAAGTATGAGCTGC 4680
Db 4621 ACGTCCCTTTCCAGTCCGCTGTGAGAGAGGAGGATTCGAAGGTGGAAGTATGAGCTGC 4680
Qy 4681 AGGAGTGTGAATCGAGAGAGAGCCCGGAGAGAGCTCAACTAGAGGTGATTAAT 4740
Db 4681 AGGAGTGTGAATCGAGAGAGAGCCCGGAGAGAGCTCAACTAGAGGTGATTAAT 4740
Qy 4741 CTGAAGCAAGAGGCAAGATTTGAACCCCGACCCCTCTTTCCAGAGTGTCT 4800
Db 4741 CTGAAGCAAGAGGCAAGATTTGAACCCCGACCCCTCTTTCCAGAGTGTCT 4800

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Db 4741 CTGAAGCAAGAGGCAAGATTTGAACCCCGACCCCACTCTTTCCAGAGTGTCT 4800
Qy 4801 GAAGAGAGTGTGTGGAGTATGAGAAAAGATGCCCTGGCCAGGACAGCATTTATGTT 4860
Db 4801 GAAGAGAGTGTGTGGAGTATGAGAAAAGATGCCCTGGCCAGGACAGCATTTATGTT 4860
Qy 4861 ACTGAACGATTTGATTTATTTTGTAAATTTCTATAAATTTTAAGAGATGACACA 4920
Db 4861 ACTGAACGATTTGATTTATTTTGTAAATTTCTATAAATTTTAAGAGATGACACA 4920
Qy 4921 TGTGTATATATAGAGAGAGATGTAAGTGTATGATCTGGGCTTTCACACTCTGCC 4980
Db 4921 TGTGTATATATAGAGAGAGATGTAAGTGTATGATCTGGGCTTTCACACTCTGCC 4980
Qy 4981 CCAGAGTGTGAGAGCCACAGAGGGGCGCTCCGATTTGTGATTTGGGCTCCGTCACA 5040
Db 4981 CCAGAGTGTGAGAGCCACAGAGGGGCGCTCCGATTTGTGATTTGGGCTCCGTCACA 5040
Qy 5041 ACCAAGCTTCAATAGTCTTAAATTTGACATATGTGCTGCTTAAATATTTATAT 5100
Db 5041 ACCAAGCTTCAATAGTCTTAAATTTGACATATGTGCTGCTTAAATATTTATAT 5100
Qy 5101 TTACTTTATATATTTCTATGCAATATTTGCTTATGTAATATTTTGTAAAGTTTC 5160
Db 5101 TTACTTTATATATTTCTATGCAATATTTGCTTATGTAATATTTTGTAAAGTTTC 5160
Qy 5161 TGTTTAAATATTTTAAATTTGATATACAAACCCCTGGTATGTAATGTTACTGTT 5220
Db 5161 TGTTTAAATATTTTAAATTTGATATACAAACCCCTGGTATGTAATGTTACTGTT 5220
Qy 5221 AACTTTCAACACGCTATGCTGATTAATTTTGTAAATGAGCAGATATGAAAGAGC 5280
Db 5221 AACTTTCAACACGCTATGCTGATTAATTTTGTAAATGAGCAGATATGAAAGAGC 5280
Qy 5281 CCGGAATT 5288
Db 5281 CCGGAATT 5288

RESULT 2
US-08-954-668-18
? Sequence 18, Application US/08954668
? GENERAL INFORMATION:
? APPLICANT: SCOTT, MATHEW P
? APPLICANT: GOODRICH, LISA V
? APPLICANT: JOHNSON, RONALD L
? TITLE OF INVENTION: Patched Genes and their use
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley, Hoag & Elliot
? STREET: One Post Office Square
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII(text)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/954,668
? FILING DATE: 20-Oct-1997
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Vincent, Matthew P.
? REGISTRATION NUMBER: 36709
? REFERENCE/DOCKET NUMBER: SUV-003.06
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-832-1000
? TELEFAX: 617-832-7000
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:

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LENGTH: 5288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 us-08-954-668-18

Query Match 100.0%; Score 5288; DB 13; Length 5288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGGACCGGAGAGAGTCCCGGGAGAGCCCGGAGAGACAGGCTCGTCGGCC 60
 Db 1 GAATTCGGGGGACCGGAGAGAGTCCCGGGAGAGCCCGGAGAGACAGGCTCGTCGGCC 60
 QY 61 GCCGCTCTGCTCTTCCGCAACGTGATGTGGGAGCGCGCGGCGGCGGAGAGACTCTGGGA 120
 Db 61 GCCGCTCTGCTCTTCCGCAACGTGATGTGGGAGCGCGCGGCGGCGGAGAGACTCTGGGA 120
 QY 121 CCCCCCGCAATGTGCAAGTGAAGCGCCAGGGCTGACTCCCGGACGCGCGCGCC 180
 Db 121 CCCCCCGCAATGTGCAAGTGAAGCGCCAGGGCTGACTCCCGGACGCGCGCGCC 180
 QY 181 GCAGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 Db 181 GCAGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 241 CGAGCCCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 Db 241 CGAGCCCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 301 GAGCCCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 Db 301 GAGCCCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 361 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 Db 361 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 QY 421 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 Db 421 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 QY 481 GCAGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 Db 481 GCAGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 QY 541 CGAGCTACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
 Db 541 CGAGCTACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
 QY 601 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
 Db 601 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
 QY 661 ACATTTAAAAAACTGCGGCAAGTTCTTGTTGGGCTCTCATATTTGGGGCTCTCG 720
 Db 661 ACATTTAAAAAACTGCGGCAAGTTCTTGTTGGGCTCTCATATTTGGGGCTCTCG 720
 QY 721 CGGTGGGATTTAAAGCGGCAACTCGAGCAACGTGGAGAGCTGGGGGAGGAATTG 780
 Db 721 CGGTGGGATTTAAAGCGGCAACTCGAGCAACGTGGAGAGCTGGGGGAGGAATTG 780
 QY 781 GAGGAGGAGTAAAGTCTGGAATTAATTAATATATCTCCAGAGATTTGAGAGAGGCTATGT 840
 Db 781 GAGGAGGAGTAAAGTCTGGAATTAATTAATATATCTCCAGAGATTTGAGAGAGGCTATGT 840
 QY 841 TTAATCTCAACTCATATGATACAGACCCCTTAAGAGAGAGGCTAATGCTCGACACAG 900
 Db 841 TTAATCTCAACTCATATGATACAGACCCCTTAAGAGAGAGGCTAATGCTCGACACAG 900
 QY 901 AAGCGCTCTACAAACCTGAGACTCGGCACTCCAGGCGCAGCGCTCATGATATCATGT 960

Db 901 AAGCGCTCTACAAACCTGAGACTCGGCACTCCAGGCGCAGCGCTCATGATATCATGT 960
 QY 961 ACAACAGGAGTGGAAATTTGGAAATTTGGTGTACAAATACAGAGACTTATCCACAGAA 1020
 Db 961 ACAACAGGAGTGGAAATTTGGAAATTTGGTGTACAAATACAGAGACTTATCCACAGAA 1020
 QY 1021 CAGGTTACATGATGATATATGATATATATATATATATATATATATATATATATATAT 1080
 Db 1021 CAGGTTACATGATGATATATGATATATATATATATATATATATATATATATATATAT 1080
 QY 1081 ACTGCTTCTGGAGAGGCGGCAATTTACAGTCTGGGAGACATACCTCTAGTAAACCTC 1140
 Db 1081 ACTGCTTCTGGAGAGGCGGCAATTTACAGTCTGGGAGACATACCTCTAGTAAACCTC 1140
 QY 1141 CTTTGGGCGGCAAACTTCGACCCCTTGGAAATTTCTCGGAGAGTAAAGAAATTAAC 1200
 Db 1141 CTTTGGGCGGCAAACTTCGACCCCTTGGAAATTTCTCGGAGAGTAAAGAAATTAAC 1200
 QY 1201 ATCAAGTGGACAGTGGGAGAAATGCTGAATAAGGCTGAGGTGTCATGTATACATGG 1260
 Db 1201 ATCAAGTGGACAGTGGGAGAAATGCTGAATAAGGCTGAGGTGTCATGTATACATGG 1260
 QY 1261 ACCGCCCTGCTCAATCCGCGCATCCAGACTGCCCGGACAGCCCGCAACAAAAT 1320
 Db 1261 ACCGCCCTGCTCAATCCGCGCATCCAGACTGCCCGGACAGCCCGCAACAAAAT 1320
 QY 1321 CAACCAAACTTGTATATATGAGGCTTGTGAATGATGTGATGTGATGTGATGTGAT 1380
 Db 1321 CAACCAAACTTGTATATATGAGGCTTGTGAATGATGTGATGTGATGTGATGTGAT 1380
 QY 1381 AGTATATGACATGAGAGAGAGATGATGTGAGTGGGAGCAAGTCAAGACAGCACTGGAA 1440
 Db 1381 AGTATATGACATGAGAGAGAGATGATGTGAGTGGGAGCAAGTCAAGACAGCACTGGAA 1440
 QY 1441 AACTGTGAGGCGCCATGCTGACAGACATGTTCCAGTTAATGATCTCCCAAGCAATGT 1500
 Db 1441 AACTGTGAGGCGCCATGCTGACAGACATGTTCCAGTTAATGATCTCCCAAGCAATGT 1500
 QY 1501 ACGAGCACTTCAAGGAGGAGTACGATATGCTCAACATCAACATGGAAGAGAGACAAAC 1560
 Db 1501 ACGAGCACTTCAAGGAGGAGTACGATATGCTCAACATCAACATGGAAGAGAGACAAAC 1560
 QY 1561 CAGCATCTGAGAGCGCTGGGAGAGACATATGAGAGGTTTCAATCAGAGTTCGCAC 1620
 Db 1561 CAGCATCTGAGAGCGCTGGGAGAGACATATGAGAGGTTTCAATCAGAGTTCGCAC 1620
 QY 1621 AGAATCTCACTCAAAAAGGCTTTCTTCCACACCAACGACGACCTGAGACATCTGAAT 1680
 Db 1621 AGAATCTCACTCAAAAAGGCTTTCTTCCACACCAACGACGACCTGAGACATCTGAAT 1680
 QY 1681 CTTTCTGAGGCTGAGTGTGATCCGCGTGGGAGGAGGCTTACTATCTGCGCTATG 1740
 Db 1681 CTTTCTGAGGCTGAGTGTGATCCGCGTGGGAGGAGGCTTACTATCTGCGCTATG 1740
 QY 1741 CCTGTACACATGCTGGCTGGGAGTGTCTCCAAAGTCCAGAGGCTGGGCGTGGCTG 1800
 Db 1741 CCTGTACACATGCTGGCTGGGAGTGTCTCCAAAGTCCAGAGGCTGGGCGTGGCTG 1800
 QY 1801 GCGTCTCTGCTGGTGTGACATGTAGTGGCTGACAGGACTGGGCGCTGTCTCATATGCGAA 1860
 Db 1801 GCGTCTCTGCTGGTGTGACATGTAGTGGCTGACAGGACTGGGCGCTGTCTCATATGCGAA 1860
 QY 1861 TTTCTTTAAAGCTGCAACACTCAAGGTTTGGCAATTTCTGCTTGGTGGTGGTGG 1920
 Db 1861 TTTCTTTAAAGCTGCAACACTCAAGGTTTGGCAATTTCTGCTTGGTGGTGGTGG 1920
 QY 1921 ATGATGTTTCTTCTGCGCCAGCGCTTCAAGTGAAGAGAGAGAGTAAAGAGATCCCT 1980
 Db 1921 ATGATGTTTCTTCTGCGCCAGCGCTTCAAGTGAAGAGAGAGAGTAAAGAGATCCCT 1980
 QY 1981 TTGAGGAGAGAGAGGAGAGGCTGGAAGCGACAGAGAGGAGGCTGCGCTCAGTCA 2040

Db 1981 TTGAGCAGAGACCGGGGAGTGCCTTGAAGCGCACAGAGCCAGCGTGCGCTCAGCTCCA 2040
QY 2041 TCAGCATGTACAGACCTTTCTTCATGGCCGGTTATCCCAATTCGCCGTCTGCGGGCT 2100
Db 2041 TCAGCAATGTACAGACCTTTCTTCATGGCCGGTTATCCCAATTCGCCGTCTGCGGGCT 2100
QY 2101 TCTCCCTCCAGGAGCGGTAGTAGGTGTTCATTTTGGCATTTGGCTTCGCTCATTTTTC 2160
Db 2101 TCTCCCTCCAGGAGCGGTAGTAGGTGTTCATTTTGGCATTTGGCTTCGCTCATTTTTC 2160
QY 2161 CTGCAATTTCTCAGCATGGATTATATGACCGGAGACAGAGACTGATATTTCTGCT 2220
Db 2161 CTGCAATTTCTCAGCATGGATTATATGACCGGAGACAGAGACTGATATTTCTGCT 2220
QY 2221 GTTTTAAAGCCCTGGCTGACGAGTAGTTCAGTTGGAACCTTAGGCTTACCGGACA 2280
Db 2221 GTTTTAAAGCCCTGGCTGACGAGTAGTTCAGTTGGAACCTTAGGCTTACCGGACA 2280
QY 2281 CACAGCAATATACCGGCTACAGACCCGCCACGTCCTACAGACAGCCACAGCTTTGGCCATG 2340
Db 2281 CACAGCAATATACCGGCTACAGACCCGCCACGTCCTACAGACAGCCACAGCTTTGGCCATG 2340
QY 2341 AAACGAGATTACATGCAATGCACTGTCCAGCTCCGACGAGTAGACGACCCACAGCC 2400
Db 2341 AAACGAGATTACATGCAATGCACTGTCCAGCTCCGACGAGTAGACGACCCACAGCC 2400
QY 2401 ACGTGTACTACACACCGCTGAGCGGGCTCCGAGATCTGTGGAGCCGTCACCGTGA 2460
Db 2401 ACGTGTACTACACACCGCTGAGCGGGCTCCGAGATCTGTGGAGCCGTCACCGTGA 2460
QY 2461 CACAGGACACCCCTCAGCTGACGAGACCCAGAGAGACAGCAAGTTCACAAAGGAGACTGCTCT 2520
Db 2461 CACAGGACACCCCTCAGCTGACGAGACCCAGAGAGACAGCAAGTTCACAAAGGAGACTGCTCT 2520
QY 2521 CCCAGTTCGCGACTCCAGGCTCCACTGCTGAGACCCGCCCTGTAGAGTAGGACACTCT 2580
Db 2521 CCCAGTTCGCGACTCCAGGCTCCACTGCTGAGACCCGCCCTGTAGAGTAGGACACTCT 2580
QY 2581 CATCTTTTGTGAGAGAGCACTATGCTCTTCTTGAACCAAAAGGCAAGGTAGTGG 2640
Db 2581 CATCTTTTGTGAGAGAGCACTATGCTCTTCTTGAACCAAAAGGCAAGGTAGTGG 2640
QY 2641 TGATCTTCTTTCTGCGCTTGTGCGGGGCTCAGCCCTTATGAGCAACCCGAGTAGAG 2700
Db 2641 TGATCTTCTTTCTGCGCTTGTGCGGGGCTCAGCCCTTATGAGCAACCCGAGTAGAG 2700
QY 2701 ACGGCGTGGACCTTACGAGCACTTGTACCTCGGGAAACAGAAATATGACTTATTTGCTG 2760
Db 2701 ACGGCGTGGACCTTACGAGCACTTGTACCTCGGGAAACAGAAATATGACTTATTTGCTG 2760
QY 2761 CACAAATTAATTAATCTTTCTTCTACAAATATATATAGTACCCAGAAAGCAGACTACC 2820
Db 2761 CACAAATTAATTAATCTTTCTTCTACAAATATATATAGTACCCAGAAAGCAGACTACC 2820
QY 2821 CGAATATCAGACACTTACTTTCAGACTACAGAGAGTTTCAAGTAACTGTAAGTATGTCA 2880
Db 2821 CGAATATCAGACACTTACTTTCAGACTACAGAGAGTTTCAAGTAACTGTAAGTATGTCA 2880
QY 2881 TGTGTGGAAGAAACAAAGAGCTTCCCAAAATGTGGCTGCACATTCACAGACTGCGCTTC 2940
Db 2881 TGTGTGGAAGAAACAAAGAGCTTCCCAAAATGTGGCTGCACATTCACAGACTGCGCTTC 2940
QY 2941 AGGAGACTCAGAGATCATTTTGAAGTGAAGTGGAAACCGGGAAATCATGSCCAAAATTT 3000
Db 2941 AGGAGACTCAGAGATCATTTTGAAGTGAAGTGGAAACCGGGAAATCATGSCCAAAATTT 3000
QY 3001 ACAAGAAATGATCAGACGATGAGTCTTGGCTTACAAACTCTGTTGTAACCGGAGCC 3060
Db 3001 ACAAGAAATGATCAGACGATGAGTCTTGGCTTACAAACTCTGTTGTAACCGGAGCC 3060
QY 3061 GCGATTAAGCCCATGACATCAGCCAGTGTGACTAAACAGGCTGTGGATGCGATGGCA 3120
Db 3061 GCGATTAAGCCCATGACATCAGCCAGTGTGACTAAACAGGCTGTGGATGCGATGGCA 3120

QY 3121 TCATTAATCCAGAGGCTTTCTACATTAACCTGAGCGGTGGGCTGACGAACGACCCCGTGC 3180
Db 3121 TCATTAATCCAGAGGCTTTCTACATTAACCTGAGCGGTGGGCTGACGAACGACCCCGTGC 3180
QY 3181 CGTATGCTGCTCCAGGACCAACATCCGAGCCACACCCAGACGAATGGGTCCAGACAAG 3240
Db 3181 CGTATGCTGCTCCAGGACCAACATCCGAGCCACACCCAGACGAATGGGTCCAGACAAG 3240
QY 3241 CCGACTACATGCTGAAACAAAGGTGAGAAATCCCGGACAGCAGACCCATGAGATGCCC 3300
Db 3241 CCGACTACATGCTGAAACAAAGGTGAGAAATCCCGGACAGCAGACCCATGAGATGCCC 3300
QY 3301 AGTTCCCTTTCTACCTAACGAGGCTGGGGGACACCTCAGACTTTGTGGAGCAATTTGAA 3360
Db 3301 AGTTCCCTTTCTACCTAACGAGGCTGGGGGACACCTCAGACTTTGTGGAGCAATTTGAA 3360
QY 3361 AAGTAAGACCATCTGACGACAACTATACGAGCCCTGGGGCTGCAATTAACCCCAAGGCT 3420
Db 3361 AAGTAAGACCATCTGACGACAACTATACGAGCCCTGGGGCTGCAATTAACCCCAAGGCT 3420
QY 3421 ACCCTTCTCTTCTTGGGAGCAGTACATCGGCTCCGCACTGGCTGCTGTTCAATCA 3480
Db 3421 ACCCTTCTCTTCTTGGGAGCAGTACATCGGCTCCGCACTGGCTGCTGTTCAATCA 3480
QY 3481 GCGTGTGTGGCTGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GCGTGTGTGGCTGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3541 CCGGAGATCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
Db 3541 CCGGAGATCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3601 TCATCGGAATCAAGCTAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 TCATCGGAATCAAGCTAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3661 GAGTGAAGTTCACCGCTTACAGTTGCTTGGCTTTCAGCGGCAATCGGCGCAAGAAAC 3720
Db 3661 GAGTGAAGTTCACCGCTTACAGTTGCTTGGCTTTCAGCGGCAATCGGCGCAAGAAAC 3720
QY 3721 GCAAGGCTGTGCTTGGCTTGGAGCAGCATGTTTGGCAACCGCTGCTGATGCGCCGCTGCTCA 3780
Db 3721 GCAAGGCTGTGCTTGGCTTGGAGCAGCATGTTTGGCAACCGCTGCTGATGCGCCGCTGCTCA 3780
QY 3781 CTCTGCTGGAGTGTCTGATGCTGCGGGATGTGAGTTGCACTTCAATTTGCAAGTATTTCT 3840
Db 3781 CTCTGCTGGAGTGTCTGATGCTGCGGGATGTGAGTTGCACTTCAATTTGCAAGTATTTCT 3840
QY 3841 TTGCTGTGCTGGAGTGTCTGATGCTGCGGGATGTGAGTTGCACTTCAATTTGCTTCCG 3900
Db 3841 TTGCTGTGCTGGAGTGTCTGATGCTGCGGGATGTGAGTTGCACTTCAATTTGCTTCCG 3900
QY 3901 TGCCTTTTGTCTTCTTTTGGACATATCTGAGAGTGTCTGACGCAACCGCTTGAACCGCC 3960
Db 3901 TGCCTTTTGTCTTCTTTTGGACATATCTGAGAGTGTCTGACGCAACCGCTTGAACCGCC 3960
QY 3961 TGCCCAACACCTGCTGAGGACACCCCGACGAGTGTGCGCTGCGCAATGCGCGCCG 4020
Db 3961 TGCCCAACACCTGCTGAGGACACCCCGACGAGTGTGCGCTGCGCAATGCGCGCCG 4020
QY 4021 ACAAGCAGAGGCTGTGATTCCTGCACTCGAGATAGTTTCCAGACGAGAGTGTAG 4080
Db 4021 ACAAGCAGAGGCTGTGATTCCTGCACTCGAGATAGTTTCCAGACGAGAGTGTAG 4080
QY 4081 GCTTCAAGCAGAGCTTTCGACATACGAGGCTGACGAGGCTGCGGAGGCTTGCACAC 4140
Db 4081 GCTTCAAGCAGAGCTTTCGACATACGAGGCTGACGAGGCTGCGGAGGCTTGCACAC 4140
QY 4141 AAGTGAATGAGGAAGCAGAAACCCGCTTTCGACCTTCCACTGCTGCTGCTGCTGCTGCTGCT 4200
Db 4141 AAGTGAATGAGGAAGCAGAAACCCGCTTTCGACCTTCCACTGCTGCTGCTGCTGCTGCTGCT 4200

[illegible]

OY	1441	AACTGTCAGCGCCCATGCGCTTCGACAGACCATGTTCCAGTTAAATGACTCCCAACCAATGT	1500
Db	1441	AACTGTCAGCGCCCATGCGCTTCGACAGACCATGTTCCAGTTAAATGACTCCCAACCAATGT	1500
OY	1501	ACGACACTCTCAAGGGGTACGAGTATGTCTACACATCAACTGGAACGAGACAAAGCGG	1560
Db	1501	ACGACACTCTCAAGGGGTACGAGTATGTCTACACATCAACTGGAACGAGACAAAGCGG	1560
OY	1561	CAGCCATCCTGGAGGCTTGCGAGAGGACATATGTGGAGGTGTTTCATCAGATGTGCGAC	1620
Db	1561	CAGCCATCCTGGAGGCTTGCGAGAGGACATATGTGGAGGTGTTTCATCAGATGTGCGAC	1620
OY	1621	AGAACTCCACTCAAAAAGGTCTTCTTCACCAACCAAGACCCCTGGAGACATCTGAAAT	1680
Db	1621	AGAACTCCACTCAAAAAGGTCTTCTTCACCAACCAAGACCCCTGGAGACATCTGAAAT	1680
OY	1681	CCTTCCTGACGTCAAGTGTATCCCGGTGGCCAGCGGACTTACTCATCTCGCCATG	1740
Db	1681	CCTTCCTGACGTCAAGTGTATCCCGGTGGCCAGCGGACTTACTCATCTCGCCATG	1740
OY	1741	CCTGCTCAACCATGCTGCGCTGGGAGTGTCCAAAGTCCAGAGGTGCGTGGGGCTGACTG	1800
Db	1741	CCTGCTCAACCATGCTGCGCTGGGAGTGTCCAAAGTCCAGAGGTGCGTGGGGCTGACTG	1800
OY	1801	GGCTCCGTGCTGTTGCGACTCTGTACGTGCGTGCAGAGCTGGGCGTGTGCTCTATGATCGGAA	1860
Db	1801	GGCTCCGTGCTGTTGCGACTCTGTACGTGCGTGCAGAGCTGGGCGTGTGCTCTATGATCGGAA	1860
OY	1861	TTTCCTTTAAGCGCTGCACAAACATCAGGTTTGGCATTTCGTGCGTCTGGATGGTGTGG	1920
Db	1861	TTTCCTTTAAGCGCTGCACAAACATCAGGTTTGGCATTTCGTGCGTCTGGATGGTGTGG	1920
OY	1921	ATGATGTTTTTTCTTCGCGCCACAGCCTTAGTAAACAGAGACAGAAATAAAAGATCCCTT	1980
Db	1921	ATGATGTTTTTTCTTCGCGCCACAGCCTTAGTAAACAGAGACAGAAATAAAAGATCCCTT	1980
OY	1981	TTGAGACACGAGACCGGGAGTGTCTGAAGCGCACAGAGAGCCAGCGTGGCCCTACGTCCA	2040
Db	1981	TTGAGACACGAGACCGGGAGTGTCTGAAGCGCACAGAGAGCCAGCGTGGCCCTACGTCCA	2040
OY	2041	TCAGCAATGTCAAGGCTTCTTCATGGCGCGTAAATCCCAATTCGCGTGGGGCGT	2100
Db	2041	TCAGCAATGTCAAGGCTTCTTCATGGCGCGTAAATCCCAATTCGCGTGGGGCGT	2100
OY	2101	TCCTCCCTCAGGACGAGGGTATGATGGTGTTCATTTTGGCATAGTTCGTCATTTTC	2160
Db	2101	TCCTCCCTCAGGACGAGGGTATGATGGTGTTCATTTTGGCATAGTTCGTCATTTTC	2160
OY	2161	CTGCAATTCCTCAGCATGATTTATATACGACGCGAGGACAGAGACTGGATATTTTCGTCT	2220
Db	2161	CTGCAATTCCTCAGCATGATTTATATACGACGCGAGGACAGAGACTGGATATTTTCGTCT	2220
OY	2221	GTTTTTCAAGGCCCTGCGCTGACAGAGTATTCAGGTTGAACCTCAGGCTCTACACCGACA	2280
Db	2221	GTTTTTCAAGGCCCTGCGCTGACAGAGTATTCAGGTTGAACCTCAGGCTCTACACCGACA	2280
OY	2281	CACAGGACATATACCGGCTACAGGCCCCCAGCCTCCTTACAGACGACAGAGCTTTGGCCATG	2340
Db	2281	CACAGGACATATACCGGCTACAGGCCCCCAGCCTCCTTACAGACGACAGAGCTTTGGCCATG	2340
OY	2341	AAAGCGAGATTAACATGACAGTCCACTGTCAGGCTCCGCGAGAGTACGAGACCCCCACACGC	2400
Db	2341	AAAGCGAGATTAACATGACAGTCCACTGTCAGGCTCCGCGAGAGTACGAGACCCCCACACGC	2400
OY	2401	ACGTGTACTACACACCGGTGAGCCGCGCTCCGAGATCTCTGTGACGCCGTACCGTGA	2460
Db	2401	ACGTGTACTACACACCGGTGAGCCGCGCTCCGAGATCTCTGTGACGCCGTACCGTGA	2460
OY	2461	CACAGGACACCTCAGCTGCGCAGAGGCCAGAGAGACACAGCTCCACAAAGGAGCTGTCT	2520
Db	2461	CACAGGACACCTCAGCTGCGCAGAGGCCAGAGAGACACAGCTCCACAAAGGAGCTGTCT	2520
OY	2521	CCCAAGTTTCGAGATTCAGCCTTCACCTGCGTCGAGGCCCTTGTTACGAAGTGAACACTCT	2580

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Db 2581 CATCTTTGCTGAGAACACTATGCTCTTCTCTTGTAAACCAAAAGCAAGGTAGTG 2640
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Db 3421 ACCCTTCTCTTCTGTGGAGAGATACATGAGCTCCGACATGCTTATGATCA 3480
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DB 5281 CCGGAATT 5288

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RESULT 4
US-08-857-636-1
Sequence 1, Application US/08857636
GENERAL INFORMATION:

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APPLICANT: Dean, Michael Carlton
APPLICANT: Hahn, Heidi Eve
APPLICANT: Wickling, Carol
APPLICANT: Christiansen, Jeffrey
APPLICANT: Zaphiropoulos, Peter G.
APPLICANT: Gallant, Mae R.
APPLICANT: Shanley, Susan Mary
APPLICANT: Chidambaram, Adirami
APPLICANT: Vorechovsky, Igor
APPLICANT: Holmberg-Lindstrom, Erika
APPLICANT: Unden, Anne Birgitte
APPLICANT: Gillies, Susan Alana
APPLICANT: Negus, Kylie
APPLICANT: Smyth, Ian Mcleod
APPLICANT: Pressman, Carol Leah
APPLICANT: Lefell, David J.
APPLICANT: Gerard, Bernard
APPLICANT: Goldstein, Alisa Miriam
APPLICANT: Mainwright, Brandon
APPLICANT: Totfgard, Rune Carl-wagnus
APPLICANT: Chenevix-trench, Georgia
APPLICANT: Bale, Allen E.
TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,636
FILING DATE: 16-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,906
FILING DATE: 17-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P00363
FILING DATE: 07-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,765
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-278200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..6568 /note= "human nevold basal cell
OTHER INFORMATION: carcinoma syndrome (NBCCS)
OTHER INFORMATION: (PATCHED (PTC)) cDNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 442..4332
US-08-857-636-1

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Query Match 88.6%; Score 4684.8; DB 12; Length 6568;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4692; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 585 GGAAGGCTACTGCGCGGAAAGCCCACTGAGCTGAGAGGAAGTTTCAGAGACTCTT 644
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DB 250 TTTAACTGGGTGTATCAATTTCAAAAAAAGTGGGCAAGTTCTTGGTGGGCTCTCTC 704
QY 705 ATATTTGGGGCTTCTGGGCTGGGATTTAAAGCAGCAAGCTCGAGACCAAGTGAAGAG 764
DB 310 ATATTTGGGGCTTCTGGGCTGGGATTTAAAGCAGCAAGCTCGAGACCAAGTGAAGAG 764
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Db 670 ATTATTACACCTTTGGAGCTGCTTGGAGAGGGGGAATTTACAGCTGGAGACGATAC 729
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QY	3165	AGCAAGCAGCCCGTCCGCTATGCTGCTCCAGGCGCAACATCCGCGCACACAGCAGCAAA	3224
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QY	3285	CCCATGAGATATGCCAGTTCCTTCTTACCTCAACGGGTTGGCGGACACCTCGACGCTT	3344
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QY	3345	GTCGAGGCAATTGAAAAAGTAAAGAACCATCTGACAGCAATATAGAGCCGTGGGCTTCC	3404
Db	2950	GTCGAGGCAATTGAAAAAGTAAAGAACCATCTGACAGCAATATAGAGCCGTGGGCTTCC	3009
QY	3405	AGTTACCCCAAGGCTTACCCCTCTCTCTCGGAGAGATACATCGGCGCTCCGACATGG	3464
Db	3010	AGTTACCCCAAGGCTTACCCCTCTCTCTCGGAGAGATACATCGGCGCTCCGACATGG	3069
QY	3465	CTGCTGCTGTTTCATCAGCCGCTGCTTGGCCCTGCACATTCCTCGCTGCTGCTGCTT	3524
Db	3070	CTGCTGCTGTTTCATCAGCCGCTGCTTGGCCCTGCACATTCCTCGCTGCTGCTGCTT	3129
QY	3525	CTGAACCCCTGAGACGGCGGGATCATTTGTATGTGCTCGCGCTGATGACGCTGACCTG	3584
Db	3130	CTGAACCCCTGAGACGGCGGGATCATTTGTATGTGCTCGCGCTGATGACGCTGACCTG	3189
QY	3585	TTGCGCATGATGGGCTCATCGGAATCAAGCTAGTGGCGGTGCCCGGTGCATCTGATC	3644
Db	3190	TTGCGCATGATGGGCTCATCGGAATCAAGCTAGTGGCGGTGCCCGGTGCATCTGATC	3249
QY	3645	GCTTCTGTTGGCATAGAGAGTGAAGTTCACCGTTACAGTTGCTTTGGCGTTTTCAGCGGC	3704
Db	3250	GCTTCTGTTGGCATAGAGAGTGAAGTTCACCGTTACAGTTGCTTTGGCGTTTTCAGCGGC	3309
QY	3705	ATCGGCGCAAGAACCGCGAGGCTGTGCTTGCCTCGAGACATGTTTTGCACCCGCTCCTG	3764
Db	3310	ATCGGCGCAAGAACCGCGAGGCTGTGCTTGCCTCGAGACATGTTTTGCACCCGCTCCTG	3369
QY	3765	GATGCGCGCTGTCACACTGCTGGGAGTGTGCTGCTGGCGGGATCTAGTTGCACTTC	3824
Db	3370	GATGCGCGCGTGTGTCACACTGCTGGGAGTGTGCTGCTGGCGGGATCTAGTTGCACTTC	3429
QY	3825	ATTGTCAGGTATTTCTTCTGCTGTGCTGCGGATCTCACCATCTCGCGCTTCTCAATGGG	3884
Db	3430	ATTGTCAGGTATTTCTTCTGCTGTGCTGCGAATCTCACCATCTCGCGCTTCTCAATGGG	3489
QY	3885	CTGGTTTGTGCTTCCGCTGCTTGTGCTTCTTGTGACATATCTGAGTGTCTCCAGCC	3944
Db	3490	CTGGTTTGTGCTTCCGCTGCTTGTGCTTCTTGTGACATATCTGAGTGTCTCCAGCC	3549
QY	3945	AACGGCTTGAAACCGCTGCGCACACACCTCCCTGAGCCACCCCGGCGGTGCGCTTC	4004
Db	3550	AACGGCTTGAAACCGCTGCGCACACACCTCCCTGAGCCACCCCGGCGGTGCGCTTC	3609
QY	4005	GCCATGCGCGCGCGCCACACGACAGCGGGTGTATTTCTCTCGACTCGGAGTATAGTTCC	4064
Db	3610	GCCATGCGCGCGCGCCACACGACAGCGGGTGTATTTCTCTCGACTCGGAGTATAGTTCC	3669
QY	4065	CAGAGACAGTGTACAGGCTTACGACGAGGCTTCCGACTACGAGGCCACGACAGGCGCG	4124
Db	3670	CAGAGACAGTGTACAGGCTTACGACGAGGCTTCCGACTACGAGGCCACGACAGGCGCG	3729
QY	4125	GGAGGCGCTGCGCCACCAAGTATCTGTGAAGCGACAGAAACCCCGCTCTTCCGCACTCC	4184

QY	1826	GGCTGAGAGACATGGGCTGTGCTGATGATGGAATTTCCCTTAACGCTGCACACATCA	1885
DB	1497	GGCTGAGAGATGGGCTCTGCTCCCTTGATGTGGCATTTCTTTAACTGCTGCACAACTCA	1556
QY	1886	GGTTTTGCCATTTTCGCGCTTTGGTGGTGGATGATGTTTTTTCTCTGGCCCCAGCG	1945
DB	1557	GGTTTTGCCGTTTCTGCTCTGGTGGTGGATGATGTTCTCTCTCTGGCCCATGCG	1616
QY	1946	CTTTCAGTGAACAAGGACACAATTAAGAATTCCTTTTGAAGAGACAGCGGGGAGTGCCT	2005
DB	1617	ATTTCAGTGAACAAGGACACAATTAAGAGATTCATTTTGAAGAGACAGCGGGGAGTGCCT	1676
QY	2006	GAAGGACAGAGAGCGAGGCTGGCCCTCACGTCCATCAGCAATGTGCAGACCTTCTTCAT	2065
DB	1677	CAAGGCGACCGGAGCGCAGGCTGGCCCTCACGTCCATCAGCAATGTGCAGACCTTCTTCAT	1736
QY	2066	GGCCGCGTTTAAATCCAAATTCGCGCTTCGGGCGCTTCTCCCTGCAGGACGGTACTAGT	2125
DB	1737	GGCCGCGTTTAAATCCAAATTCGCGCTTCGGGCGCTTCTCCCTGCAGGACGGTACTAGT	1796
QY	2126	GGTTGTTCAATTTTGGCATGCTGCTGCTCATTTTCTTGCAATTCACGATGATTTATA	2185
DB	1797	GGTATTTCATTTTGGCATGCTGCTGCTCATTTTCTTGCAATTCACGATGATTTATA	1856
QY	2186	TCGACGCGAGGAGAGAGAGATGATATTTTCTGCTTTTACAAAGCCCTGCTGCAGACG	2245
DB	1857	CAGAGGTGAGGACAGAAAGATTTGGATTTTCTGCTGCTTTACAGAGCCCTGTGTGACGAC	1916
QY	2246	ACTGATTCAGGTTTGAACCTTCAGGCTTCACCGACACACAGCAATACCCTGCTACAGCC	2305
DB	1917	GCTGATTCAGGTTTGAAGCTTCAGGCTTCACCGACACAGCAATACCCTGCTACAGCC	1976
QY	2306	CCCACTCTCCCTACAGAGGCGACAGGCTTGGCCATGAAGCGAGATTACATGCAATGCCAC	2365
DB	1977	CCCACTCTCCCTACAGAGGCGACAGGCTTGGCCATGAAGCGAGATTACATGCAATGCCAC	2036
QY	2366	TGTCAGAGCTCCGACGAGATAGACCCCGACAGCGACGTACTACACACCGCTAGACG	2425
DB	2037	GCTTCAGGCTCCGACAGAGATAGACCCCGACAGCGAGTACTACACACCGCCCGACGC	2096
QY	2426	GGGCTTCGAGATCTCTGTGACAGCCGCTCACCGTACAGACAGACACCTGACGTCCAGAG	2485
DB	2097	AGCGCTGTGATCTCTGTACAGCCTGTTTACCGTACCCAGGACAACTCAGCTGTCTAGAG	2156
QY	2486	CCCAAGAGACACAGCTCCACAAGGAGCCTGCTCCCGAGTTCTCCGATCCAGCCCTTCA	2545
DB	2157	TCCCGAGACACACAGCTCTACAGGAGCTGCTCTCCAGTTCTCAGACTCCAGCCCTTCA	2216
QY	2546	CTGCTTCGAGCCCGCTGTACGAAAGTGAACACTCTCATTTTGTGAGAAAGACTATGCG	2605
DB	2217	CTGCTTCGAGCCCGCTGTGACCAAGTGAACACTCTCTGTTTGCAGAAAGACACTATGCG	2276
QY	2606	TCTTTTCTCTTTGAACCAAAAGCCAGAGTACTGTTGATCTTCTTTTCTGGGCTTGGCT	2665
DB	2277	TCTTTTCTCTCTTTGAACCAAAAGCCAGAGTACTGTTGATCTTCTTTTCTGGGCTTGGCT	2336
QY	2666	GGGGGTTCAGCCCTTATGGGACACCGCGAGTGAAGAGCGGGCTGGACCTTACGGACATTTGT	2725
DB	2337	GGGGGTTCAGCCCTTATATGGGACACCGCGAGTGAAGAGCGGGCTGGACCTTACGGACATTTGT	2396
QY	2726	ACCTTGGGAAACAGAGAATATGACTTTATTTGTCACAAATTCAAATACTTTTCTTTCA	2785
DB	2397	TTCGCGGGAAACAGAGAATATGACTTTATTTGTCACAAATTCAAATACTTTTCTTTCA	2456
QY	2786	CAACATGTATATAGTCCACAGAAAGACACTACCCGAATATCCAGACCTTACTTTACGA	2845
DB	2457	CAACATGTATATAGTCCACAGAAAGACACTACCCGAATATCCAGACCTTACTTTACGA	2516
QY	2846	CTTACACAGAGATTCTAGTAAGCTAAGTATGTCACTGTTTGAAGAAACAAACAGCTTGC	2905
DB	2517	CTTACATTAAGAGTTTACCAATGTGAAGTATGTCACTGCTGGAAGGAACAAACAGCTTGC	2576
QY	2906	CAAAATGTGGCTGCACACTCTTCAGAGACTGGGCTTCAGGAGACTTCAGAGATTTGACAG	2965
DB	2577	CCAAATGTGGCTGCACACTTTTGAAGACTGGCTTCAAGGACTTCAGAGATTTGACAG	2636
QY	2966	TGACTGGGAAACCGGAAAAATCATATGCCAAATTTACAAATATGATCAGACATGAGAT	3025
DB	2637	TGACTGGGAAATCGGAGAGATTCATGCCAAATTTTAAAAATATGATCAGATGACGGGCT	2686
QY	3026	CTTTGCTTACAAACTCTGTGTGCAAAACCGGACCGCGATTAAGCCATTCAGATCAGCCA	3085
DB	2697	CTTTCGTTTACAAACTCTGTGTGTGAGACTGTGCAGCGGAGCAAGCCCATTCGACATTTATGCA	2756
QY	3086	GTTGACTAAACAGAGTGTGTGTGATGAGATGATTAATATCCAGCCCTTCTTCAT	3145
DB	2757	GTTGACTAAACAGAGTGTGTGTGATGAGATGATTAATATCCAGCCCTTCTTCAT	2816
QY	3146	CTACCTGACGCTTGGGTGACAGCAAGCAACCCGCTGATGCTTCCCTCCAGGCGCAAT	3205
DB	2817	CTACCTGACGCTTGGGTGACAGCAAGCAACCCGCTGATGCTTACGCTGCGCTCCAGGCGCAAT	2876
QY	3206	CCGGCCACACCGACAGCAAAATGGGTTCCAGCAACAAAGCCGACTACATGCTGCAACAGGCT	3265
DB	2877	CCGGCCCTACCGGCGGAGTGGGTTCCATGACAAAGCCGACTACATGCTGCAACAGGCT	2936
QY	3266	GAGAATCCCGGACAGAGGCCCATCGAGTATGCGCAGATTCCTTCTTACCTCAACGGGTT	3325
DB	2937	GAGAATCCCGACAGAGGCCCATCGAGTATGCGTCACTTCCCTTTCTACCTCAACGGGCT	2996
QY	3326	GGGGGACACCTTCAGACTTTTGGAGGCAATTTGAAGACCATTCGACAGCACTA	3385
DB	2997	ACGAGACACCTTCAGACTTTTGGAGGCAATTTGAAGACCATTCGATGTAACACTA	3056
QY	3386	TACGAGCCTTGGGCTGTCCAGTTAACCCCAACGGGCTACCCCTTCTCTTCTGGAGACGTA	3445
DB	3057	TACGAGCCTTGGGACTGTCCAGTTAACCCCAATGGCTTACCCCTTCTTCTTGGAGACATA	3116
QY	3446	CATCGGCTCCGCGCACGTGGCTGTGCTGCTTCAATCAGAGGTGTGGCTGSCATATTCCT	3505
DB	3117	CATCAGGCTCCGCGCACGTGGCTGTGCTGCTTCAATCAGAGGTGTGGCTGSCATATTCCT	3176
QY	3506	CGTGTGCGCTGTCTTCTTCTTGAACCCCTGGAGCGCGGAGTATGTGATGTTCTGCG	3565
DB	3177	AGTGTGCGGCTTCTTCTTCTTGAACCCCTGGAGCGCGGAGTATGTGATGTTCTGCG	3236
QY	3566	GCTGATGACGCTGAGACTGTTCGGCATGATGGGCTCATGTGGAAATCAAGCTACGTGCGCT	3625
DB	3237	TCTGATGACCGCTTGTGATGAGTGGGCTCTCATTTGGGATCAAGCTGATGCTGTGT	3296
QY	3626	GGCCGTGATCATCTGATGCTCTCTGTGGCATAGAGTGTGATTCACCGTTCACGTTGC	3685
DB	3297	GCTGTGTGATCATCTGATGCTCTCTGTGGCATAGAGTGTGATTCACCGTTCACGTTGC	3356
QY	3686	TTTTGGCTTTTTCGAGCGGCATCGGCGAAGAAACCGAGGGCTGTGCTTGGCCCTGAGCA	3745
DB			

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Db 3657 TCCAACTGTCGTCGGTTTCCCTGCTCCTGTCACAGCAAAAGTGTGATTCCTC 3716
Qy 4046 CGACTCGGAGTAAATATTCCTCCAGACAGACAGTGTACGCTCAGCAGAGGCTTGGCACTA 4105
Db 3717 CGACTCGGAGTAAATATTCCTCCAGACAGACAGTGTGTGATGTATGAGAGCTCAGGCAATA 3776
Qy 4106 CGAGGCCGACGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4165
Db 3777 CGAAGCCAGCAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 3836
Qy 4166 CCCCCTCTTCCGCACTACAGTGTGTCATCCGCAATCCAGCATACCCACCCTTGAA 4225
Db 3837 CCGTCTCTTCCGCACTACAGTGTGTCATCCGCAATCCAGCATACCCACCCTTGAC 3896
Qy 4226 CCGGAGACAGCAGCCCTCAGACTGAGGTCCTGCTCCGAGCAGGAGGCGGAGCA 4285
Db 3897 CCGTCTGAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 3956
Qy 4286 GCGCCGAGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4345
Db 3957 GCGTCTGAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4016
Qy 4346 GCGTCTGAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4405
Db 4017 GCGTCTGAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4076
Qy 4406 TCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4465
Db 4077 CCGTCTGAGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4136
Qy 4466 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4525
Db 4137 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4196
Qy 4526 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4581
Db 4197 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4250
Qy 4582 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4636
Db 4251 TCGAGAGCTACCTGAGAGCTGATGACGAGGAGGCTTGGCCACCAAGATGATGTTGAGAG 4310
Qy 4637 CCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4696
Db 4311 CAGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4370
Qy 4697 GCGGCGGAGGAGGCGGGGAGGCTTGGCCACCAAGATGATGTTGAGAGCCACAGAAAA 4756
Db 4371 GCGGAGGAGGCGGGGAGGAGCTCCTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 4430
Qy 4757 AAGAGTTGAGAAACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4816
Db 4431 AAGAGTTGAGAAACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4489
Qy 4817 AGTTATGAGAAAGATGCGCTGTGCGAGAGCAGAGTTCACTGTTAACCAGATTGTA 4876
Db 4490 AATTATG-----GGAAGGAGGAGTTCACTGTTAACCAGATTGTA 4530
Qy 4877 TATTTTGTAAATATTTCTATAAATATTTAAGAGATGATACATGTTAATATGAGAG 4936
Db 4531 TATTTTGTAAATATTTCTATAAATATTTAAGAGATGATACATGTTAATATGAGAG 4588
Qy 4937 GAAGATGTAAGTGTATGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4996
Db 4589 AATATGCTGATACAGT-CTAATTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4647
Qy 4997 AAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5056
Db 4648 ACA--GGGCGCTTCCCTGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 4705
Qy 5057 CTTAAA-----TTTCAGCATATGTTGCTGCTGTTAATATGTTAATATTTACTTGT 5108
Db 4706 TTTTAAAAAAATCTCCAGCATATGCTGCTGCTTAAATATGTTAATATTTACTTGT 4765

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Qy 5109 ATATTTATGCAAAATATTTGCTTATGTAATAGATTAATTTGTAAGGTTTCTGTTAAA 5168
Db 4766 ATAAATTCATGCAAAATATTTGCTTATGTAATAGATTA-TTTGTAAAGTTTCTGTTAAA 4824
Qy 5169 ATATTTAATTTGATATACACACCTTGTGTAGTATGTAATTTACTGTTAATTTGTA 5228
Db 4825 ATATTTAATTTGATATACACACCTTGTGTAGTATGTAATTTACTGTTAATTTGTA 4884
Qy 5229 AACAGCTATGCTGATATTTTGTAAAGCAGATATGAGAAAGC 5280
Db 4885 AACAGCTATGCTGTA-----TTGTTAAAGCAGATGAGAAAGC 4931

RESULT 6
US-08-954-655-9
? Sequence 9, Application US/08954655
? GENERAL INFORMATION:
? APPLICANT: SCOTT, MATHEW P
? GOODRICH, LISA V
? JOHNSON, RONALD L
? TITLE OF INVENTION: Patched Genes and their use
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley Hoag & Eliot
? STREET: One Post Office Square
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII(text)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/954,655
? FILING DATE: 20-Oct-1997
? CLASSIFICATION: <unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Vincent, Mathew P.
? REGISTRATION NUMBER: 36709
? REFERENCE/DOCKET NUMBER: SUV-003.06
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-832-1000
? TELEFAX: 617-832-7000
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5187 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-954-655-9

Query Match 71.9% Score 3801.2; DB 13; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;
Qy 446 CCGTCCCGCGGAGCGGCTGTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 505
Db 120 CGGGGCCCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179
Qy 506 TCGTCCCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 565
Db 180 C---GCGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
Qy 566 TCTGAGCAGATTTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 625
Db 237 TCTGAGCAGATTTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 296

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QY	626	GAAAGTTTCAGAGACTCTTATTATTTAAACCTGGGTTGTACATTCATAAAAAAACTCGCGCAAGTT	685
Db	297	GAAAGTTTCAGAGACTCTTATTATTTAAACCTGGGTTGTACATTCATAAAAAAACTCGCGCAAGTT	356
QY	686	CTTGCTGTGGGCCCTCCATATTTTGGGGCCCTGCGGTGGGATTTAAAGCAGCAAGCAACT	745
Db	357	TTTTGGTTGGGCTCTCCATATTTTGGGGCCCTTGCTGTGGGATTTAAAGCAGCAAGCAACT	416
QY	746	CGAGACCAACAGCTGAGGAGACTGTGGGTGGAACTTGGAGGACAGAGTAACTGTGAATTTAA	805
Db	417	CGAGACCAACAGCTGAGGAGACTGTGGGTGGAACTTGGGTGAGACAGTAACTGTGAATTTAA	476
QY	806	TTATATCGCCCAAGAAATTGGAGAGGCTATTGTTTAATCCTCAACATCATATTCACAG	865
Db	477	TTATATCCCTCGAAGATATGGAAGAGGCTATTGTTTAATCCTCAACATCATATTCACAG	536
QY	866	CCCTTAAGCAGAAGGTGCTAATGTCTGTGACACAGAAAGGCTCTCAACAACACTTGACTTC	925
Db	537	TCCAAAGAAAGAGGGGCTAATGTCTGTGACACAGAGGCTCTCTGCAACACTTGACTTC	596
QY	926	GGCACTCCAGGCCAGCCGTGCTCATGTATACATGTACACAGCGAGTGAATTTGGAAACA	985
Db	597	ACCACATCCAGGCCAGCGTGCTGACCTGTACATGTATACAGCGAATGGAAGTTGGAACA	656
QY	986	TTTTGTATTCAAAATCAGAGAGCTTTTCACAGAAACAGGTTACATGATCAGATTAATAGA	1045
Db	657	TTTTGTCTCAAAATTCAGGGGAACTTATCAGGGAGACAGGTTACATGATCAGATTAATAGA	716
QY	1046	ATATCTTTACCCCTGTGTTGATTAATTAACACCTTTGGACTGCTTCTGGGAAGGGGCCAAAT	1105
Db	717	ATATCTTTACCCCTGTGTTGATTAATTAACACCTTTGGACTGCTTCTGGGAAGGGGCCAAAGCT	776
QY	1106	ACAGCTGTGGACAGCAATACCTCTAGTAAACCTCTCTTGGGTGGACAAACTTTGCAGACC	1165
Db	777	ACAGCTGTGGACAGCAATACCTCTAGTAAACCTCTCTTGGGTGGACAAACTTTGTACACC	836
QY	1166	TTTGTGAATTCCTGGAAGAGTTAAAGAAATTAACATATCAAGTGGACAGCTGGGAGGAAAT	1225
Db	837	CTTGTGAATTCCTGGAAGAGTTAAAGAAATTAACATCAAGTGGACAGCTGGGAGGAGAAAT	896
QY	1226	GCTGAATAAGGCGTGGAGTTGGTGTATGGTTTCAATGGACCGGCCCTGCTCAATCCGGCCGA	1285
Db	897	GCTGAATAAGGCGGAGTTGGTGTATGGTTTCAATGGACCGGCCCTTGCTCAACCCAGCCGA	956
QY	1286	TTCCAGACTGCCCCGCCACAGCCCCCAACAAAAATTCACCAAACTCTTGATATATGGCCCT	1345
Db	957	CCGAGATTTGCCCTGCCACAGCCCCCTTAACAAAAATTCACCAAACTCTTGATATATGGCCCT	1016
QY	1346	TGTTTTAATGGTGATGTGATGGCTTATGCAAGAAATATATGCACTGGGAGGAGAGTT	1405
Db	1017	TGTTTTAATGGTGATGTGATGGCTTATGCAAGAAATATATGCAAGAGTATATGCAATTGGCAGAGAGTT	1076
QY	1406	GATTGTGGGTGGCCACAGTCAAGAACAGCACTGGAAAACTGCTACAGCGCCCATATGCCCTGCA	1465
Db	1077	GATTGTGGGTGGTACGCTCAAGAAATGGCACATGGAAAACTGTGACGCCCTCACAGCGCCCTGCA	1136
QY	1466	GACCATGTTCACGTTAATAGTCTCCCAAGCAAAATGTACAGACACTTCAAGGAGTTCAGACTA	1525
Db	1137	AACCATGTGTCCAGTTAATAGTCTCCCAAGCAAAATGTATGACACTTTCAGGGGCTACGACTA	1196
QY	1526	TGTTCTACACATCACTAAGTGAAGCAGAGCAAAAGCGGACGCACTCTGGAAGGCTTGGCAGAG	1585
Db	1197	TGTCTCTACATCAACTGTGAATGGAAGCAGAGCGCGCCCATCTGGAAGGCTTGGCAGAG	1256
QY	1586	GACATATGTGAGAGTGGTTCAATCAGAGTGTGCGCACAGAACTGCACCTCAAAAAGTGTCTTC	1645
Db	1257	GACTTACGTGAGAGTGGTTCAATCAAAAGTGTGCCCCAAACTGCACCTCAAAAAGTGTCTTC	1316
QY	1646	CTTCAACCCAGCAAGCCCTGGACAGCAATCTGAAATCTCTTCTGACGTCAGTGTCAATCG	1705
Db	1317	CTTCAACACACAGACCCCTGGACAGCAATCTGAAATCTCTTCTGATGTCAAGTGTCAATCG	1376
QY	1706	CGTGGCCACGGGCTACTTACTATCTGCTCCCTATGCTGTCAACATGCTGCGCTGGGA	1755

Db	1377	ACTGGCCAGCGGCTACCTACCTAGATGCTTGGCCATGCCCTGTTTAACCACTGCTGCCGTGGGA	1436
QY	1766	CTGGCTCAAGTCCACAGGTTGCCGTGGGCTGGCTGGGCTCTGGCTGGTTGGACATGTCAGT	1825
Db	1437	CTGCTCCAAAGTCCCGAGGGTGGCGTGGGGCTGGCTGGGCTCTGGTTGGTTGGCTCAGT	1496
QY	1826	GGCTCAGAGACTGGGCTGTGGCTCTCATATGACGGAAATTTCTCTTAAAGCTGCAACACCA	1885
Db	1497	GGCTCAGAGATTTGGGCTCTGCTCTGATTGGCAATTTCTTTAATGCTGGCACAACATCA	1556
QY	1886	GGTTTGGCCATTTCGTGCTTTGGTTGGTGGTGGATGATGTTTCTTTCTTGGCCACAGC	1945
Db	1557	GGTTTGGCCGTTTCTTGCTCTTGGTTGGTGGTGGATGATGATCTTCTCTCGGGCCATGTC	1616
QY	1946	CTTCAGTGAACAGGACAGAAATAAAGAAATCCCTTTTGGAGCAGAGCCGGGAGGTGCT	2005
Db	1617	ATTCACTGAACAGGACAGAAATTAAGAGATTCATTTTAGAGACAGAGCTGGGAGATGGCT	1676
QY	2006	GAAGCGCACAGGAGCCAGCGTGGCCCTCAGCTCATCAGCAATGTCACAGCCTTCTTCAT	2065
Db	1677	CAAGGCGACCGGAGCGCAGCGTGGCCCTCAGCTCATCAGCAATGTCACAGCCTTCTTCAT	1736
QY	2066	GGCCCGGTTAATCCCAATTCGCCGCTGGGGGGGTTCTCCCAAGGGAGCGGTAGTACT	2125
Db	1737	GGCCCGATTGATCCCTCATCTCTGGCCCTGGAGGGTCTCTCCCAAGGCTGCTGTGGTGGT	1796
QY	2126	GGTGTTCAAATTTTGGCATGTTCTGTCTCATATTTTCTGTCAATTTTCAGCATGGATTTATA	2185
Db	1797	GGATTTCATTTTGCATATGTTGTGTGTGTCTCATATTTTCTGTCAATTTTCAGCATGGATTTATA	1856
QY	2186	TCGACGCGAGGACAGAGACTGATATTTTTCGTGCTTTTACAGGCCCTGGCTCAGCGAG	2245
Db	1857	CACACGCTGAGGACAGAAAGATTGGATATTTTCTGCTTTTCACAGGCCCTGTCTCAGCAG	1916
QY	2246	AGGATATTCAGGTTGGAACCTCAGGCTTCACCGACACACAGCAATTAACCGGCTACAGGCC	2305
Db	1917	GGTGAATTCAGTTGAGCCACAGGCTTCACACAGAGCTCACAGTAACACCGGGTACAGGCC	1976
QY	2306	CCCACCTCCCTACAGCACCCACAGCTTTGGCCATGAAGACGACATTAACATGCATGCTCAC	2365
Db	1977	CCCACCCCATATCACACGACACAGCTTGGCCCAAGAAACCAATATCATATTGCAATGTCAC	2036
QY	2366	TGTCCAGCTCCGACGAGTAGACACCCCGACAGGACGTTACTACACACCCGCTAGGCC	2425
Db	2037	CGTTACACTCCGACAGAGTATGACCCCTCACAGCAGCTTACTACACACCCGCTAGGCC	2096
QY	2426	GGCTTCGAGATCTCTGTGAGCCCGCTCACCGTAGACACAGGACCCCTCAGCTCAGAG	2485
Db	2097	ACGCTCTGAGATCTCTGTACAGCTCTGTATACCGTACCCAGAGAACCTCAGCTGTACAG	2156
QY	2486	CCCAGAGACACACAGCTTCACAAAGGAGACGTCCTCCACATTCGTCGACATCCAGCCCA	2545
Db	2157	TCCCGAGAGACACAGCTCTCACACAGGAGCTGTCTCCCAATGTTCTCAGACTCCAGCTCCA	2216
QY	2546	CTGCTCGAGAGCCCGCTGTACGAGTGGACACTCTACTTTTGTCTGAGAGCACTATGTC	2605
Db	2217	CTGCTCTGAGGCCCCCTGACACCAAGTGGACACTCTTCGTTTCAGAGAAAGCACTATGTC	2276
QY	2606	TCCTTTCTCTTGAACCAACCAAGCCAAAGTAGTGTGATCTTCTCTTTCTGGGCTTGGCT	2665
Db	2277	TCCTTTCTCTCTGAAACCCCAAAAGCCAAAGTTGTGTGTAATCTTTTCTCGGGCTTGGCT	2336
QY	2666	GGGGGTGAGCCCTTATGGACACACCCGAGTAGAGAGGGGCTGGACCTTATAGCAATGTT	2725
Db	2337	GGGGGTCAAGCTTTATGGAGCACACCCGAGTAGAGAGGGGCTGGACCTCAAGCAATGTT	2396
QY	2726	ACCTCGGGAACACAGAAATATGACTTATTTGTCTGCACAAATTCATTAATCTTTCTTTCTA	2785
Db	2397	TCCCGGGAAACACAGAAATATGACTTATGCTAGCTCCAGTTTCAAGTAAATCTTCTTTCTA	2456
QY	2786	CACATGTATATAGTCAACCCAGAAAGCAACTACCCGAAATTCAGAGCACTTACTTTACGA	2845

Db 2457 CAACATGTATATAGTCACCCAGAAAGACACTACCCGAATATCCAGCACTACTTTACGA 2516
QY 2846 CCTACACAGAGATTTCAGTAACGTGAAGATATGTATGTGGAAGAAACAAACAGCTTCC 2905
Db 2517 CCTCATTAAGAGTTTCACACAAATGTGAAGATGTGATGCGGAGAGAAACAAACAGCACTTCC 2576
QY 2906 CAAATATGGGCTGCACACTACTTCAGAGACTGGCTTCAGAGGACTTCAGAGATGCAATTTGACAG 2965
Db 2577 CCAATATGGGCTGCACACTACTTCAGAGACTGGCTTCAGAGACTTCAGAGATGCAATTTGACAG 2636
QY 2966 TGACTGGGAACCGGAGAAATCATGCAAAACAATTCAAAGATGATGATGACAGATGAGAT 3025
Db 2637 TGACTGGGAACCGGAGAGATCATGCCAAACATTTATAAAAATGATGATGATGAGAGAT 2696
QY 3026 CATTGCTTACAACTCCTGTGTGCAAAACCGGAGCCGCGATTAAGCCATGACATGACCA 3085
Db 2697 CATTGCTTACAACTCCTGTGTGCAAAACCGGAGCCGCGATTAAGCCATGACATTAATGTA 2756
QY 3086 GTTGAATTAACAGGCTGTGGTGTGATGCAATGCGATGCGATTCATTAATCCAGCGCTTTCACAT 3145
Db 2757 GTTGAATTAACAGGCTGTGGTGTGATGCAATGCGATGCGATTCATTAATCCAGCGCTTTCACAT 2816
QY 3146 CTACTGACGCTTGGGTGACAGCAAGCCGCGATGATGCTGCTCCAGGCGCAACAT 3205
Db 2817 CTACTGACGCTTGGGTGACAGCAAGCCGCGATGATGCTGCTCCAGGCGCAACAT 2876
QY 3206 CCGGCAACACCGAGCAAGATGGTCCAGCAAGCCGCGATGATGCTGCTCCAGGCGCAACAT 3265
Db 2877 CCGGCAACACCGAGCAAGATGGTCCAGCAAGCCGCGATGATGCTGCTCCAGGCGCAACAT 2936
QY 3266 GAGAAATCCGCGAGCAGAGCCCATGAGTATGCGCCAGTTCCTCTTCTACCTACAGCGGT 3325
Db 2937 GAGAAATCCGAGCAGCAAGCCCATGAGTATGCTGATGCTTCCCTTCTACCTACAGCGGT 2996
QY 3326 GCGGAGACACTCAGACTTTGTGAGGCAATGAAAAAGTAAAGACATCTGACAGCACTA 3385
Db 2997 ACAGACACACTCAGACTTTGTGAGGCAATGAAAAAGTAAAGACATCTGACAGCACTA 3056
QY 3386 TAGAGGCTTGGGCTGTCCAGTATACCCCAAGCGCTTACCCTTCTCTTCTGAGGAGCACTA 3445
Db 3057 TAGAGGCTTGGGCTGTCCAGTATACCCCAAGCGCTTACCCTTCTCTTCTGAGGAGCACTA 3116
QY 3446 CATGCGCTTCCGACACGCTGCTGTTCATGAGGCTGTGTTGGCTGTGGCTGACACTTCT 3505
Db 3117 CATGCGCTTCCGACACGCTGCTGTTCATGAGGCTGTGTTGGCTGTGGCTGACACTTCT 3176
QY 3506 CGTGTGCGCTGTCTTCTTGTGAACCCCTGAGACGCGGAGTCAATGATGATGCTTCTGAC 3565
Db 3177 AGTGTGCGGAGTCTTCTCTCTGAACCCCTGAGACGCGGAGTCAATGATGATGCTTCTGAC 3236
QY 3566 GGTGATGAGGCTGAGAGCTGTTCGGCATGATGGGCTCATCGGAATCAAGCTCAGTCCGT 3625
Db 3237 TGTGATGAGCCTGTGAGCTCTTGTGCAATGATGGGCTCATGAGGATCAAGCTCAGTCTGT 3296
QY 3626 GCCCGTGTGATCAGCTGCTTCTGTGATGAGAGTGAAGTTCACCGCTTCAAGTTCACGTTGC 3685
Db 3297 GCGTGTGATCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3356
QY 3686 TTTGGGCTTTCAGCGGCAATGCGGCAAGAAACCGAGGAGCTGTGCTTGGCTTGGAGCA 3745
Db 3357 TTTGGGCTTTCAGCGGCAATGCGGCAAGAAACCGAGGAGCTGTGCTTGGCTTGGAGCA 3416
QY 3746 CATGTTTGAACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3805
Db 3417 CATGTTTGAACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3476
QY 3806 GCGATTCGATTCAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3865
Db 3477 AGGATTCGATTCAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3536
QY 3866 CCGGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3925
Db 3537 CTTGGGAGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3596
QY 3926 TCCGTGAGGTGTCTCAGCAACCGCTTGAACCGCTTGAACCGCTTGAACCGCTTGAACCGC 3985
Db 3597 TCCGTGAGGTGTCTCAGCAACCGCTTGAACCGCTTGAACCGCTTGAACCGCTTGAACCGC 3656
QY 3986 CCCGAGCGTGTGCGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4045
Db 3657 TCCGAGTGTGTGCGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3716
QY 4046 CGACTGGAATTAATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4105
Db 3717 CGACTGGAATTAATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3776
QY 4106 CGAGGCGCCAGAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4165
Db 3777 CGAGGCGCCAGAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3836
QY 4166 CCGCGTCTTGGCGCACATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4225
Db 3837 CCGCGTCTTGGCGCACATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3896
QY 4226 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4285
Db 3897 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3956
QY 4286 GCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4345
Db 3957 GCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4016
QY 4346 CCGCTTTTGAATTTTCTACTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4405
Db 4017 CCGCTTTTGAATTTTCTACTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4076
QY 4406 TCGGCGGCGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4465
Db 4077 CCGGCGGCGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4136
QY 4466 GCGGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4525
Db 4137 GCGGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4196
QY 4526 GCAACCGCGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4581
Db 4197 GCAACCGCGCGCTTCTCAGCAACCTCGGAACCCAGCGTCCATGCGATGCGAGCTCCGT 4250
QY 4582 -----GCTACCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4636
Db 4251 TGAAGAGCTACCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4310
QY 4637 CCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4696
Db 4311 CAGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4370
QY 4697 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4756
Db 4371 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4430
QY 4757 AAAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4816
Db 4431 AAAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4489
QY 4817 AGTTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4876
Db 4490 AATATATG-----GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4530
QY 4877 TTAATTTGTAATTAATTTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4936
Db 4531 TTAATTTGTAATTAATTTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4588
QY 4937 GAAGATGTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4996
Db 4589 AATATGCTTACAGT--CTAATTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4647

Accession	Sequence	Position
QY 4997	ACAGTGGGGCGTCGCGTATTTGGCATTTGGGTCGCGTCCAAACCAAGCTTCATTTAGT	5056
Db 4648	ACA - GGGGCGCTTTGCCCTGTACATTTGCTCTGTGCCAACCAAGCTTAACCTAG	4705
QY 5057	CTTTAAA - - - - - TTTGACGATATGTTGCTGCTGCTTAATAATTTGTATATTAATTTACTGT	5108
Db 4706	TTTTTAAAAAAATATCTCCACACATATGTCGCTGCTGCTTAATAATTTGTATAATTTACTGT	4765
QY 5109	ATTATTTCTATGCAAAATTTGCTCTTATGTAATAGAGATTATTTGTAAAGCTTCTCGTTTAAA	5168
Db 4766	ATAATTTCTATGCAAAATTTGCTCTTATGTAATAGAGATTTA - TTTGTAAAGCTTCTCGTTTAAA	4822
QY 5169	ATTATTTTAAATTTGCATATACAAACCCCTGTGTAGTATGAATGTATCTGTAACTTCCA	5222
Db 4825	ATTATTTTAAATTTGCATATACAAACCCCTGTGTAGATGATGATTTCTTACGTTAAACCTTTTG	4884
QY 5229	AACACGCTATGCGTATGAATTTTGTGTTTAAATGACAGATATGAAGAAGC	5280
Db 4885	AACACGCTATGCGTATGA - - - - - TTTGTTTAAAGACGACATGATGAAGAAAC	4931

RESULT 7
US-08-954-668-3
; Sequence 3, Application US/08954668

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1  APPLICANT: SCOTT, MATHEW P
2  APPLICANT: GOODRICH, LISA V
3  APPLICANT: JOHNSON, RONALD L
4  TITLE OF INVENTION: Patched Genes and their Use
5  NUMBER OF SEQUENCES: 19
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Foley, Hoag & Elliot
8  STREET: One Post Office Square
9  CITY: Boston
10 STATE: MA
11 COUNTRY: USA
12 ZIP: 02109
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: ASCII(text)
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US//08/954,668
20 FILING DATE: 20-Oct-1997
21 CLASSIFICATION: 530
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Vincent, Matthew P.
24 REGISTRATION NUMBER: 36709
25 REFERENCE/DOCKET NUMBER: SUV-003.06
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 617-832-1000
28 TELEFAX: 617-832-7000
29 INFORMATION FOR SEQ ID NO: 3:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 5187 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: CDNA
36
37 US-08-954-668-3

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Query Match	71.9%	Score 3801.2	DB 13	Length 5187
Best Similarity	88.18%	Pred. No. 0		
Matches 4276: Conservative	3	Mismatches	516	Indels 57
				Gaps 11

[illegible]

Db	180	C	-GCCGGCCGGAGACCGGGAGCTATCTGACACGGGCCACACTACCTGAGACGCCCTCTTGGC	236
Qy	586	TC	TGAGACGAGATTTTCCAAAGGGGAAAGCTACTGGACCGGAAAGGCCACTGTGCGCTGAGAGC	625
Db	237	TC	TGAGACGAGATTTTCCAAAGGGGAAAGCTACTGGACCGGAAAGGCCCTGTGCGCTGAGAGC	236
Qy	626	GA	AGTTTCAGAGACTCTTATTTTAACTGGGTTGTATCAATTCAAAAAATCGCGCAAGTT	685
Db	297	GA	AGTTTCAGAGACTCTTATTTTAACTGGGTTGTATCAATTCAAAAAAGCTCGCGCAAGTT	356
Qy	686	CT	TGTGTGTGGGCGCTCCCATATTTTGGGGCGTTTGGGGTGGATTTAAACACGACGAACT	745
Db	357	TT	TGTGTGTGGGCTCTCCTATATTTTGGGCTTCGCTGTGGGTTTAAAGCAGCTAATCT	416
Qy	746	CG	AGACCAACGTCGAGAGACTGTGGCTGGAAAGTTGAGAGACGAGTAAGTCGTAATTTAA	805
Db	417	CG	AGACCAACGTCGAGAGACTGTGGGGAAGTTGGTGACGAGTGCAGTGCAGATTTAA	476
Qy	806	TT	TATATCTGCCACAGATTTGGAGAAAGGCTATGTTTAACTCCATCACTCATGTATACGAC	865
Db	477	TT	TATATCCCTCCAGAAATATAGGAAGAAAGGCTATGTTTAACTCCATCACTCATGTATACGAC	536
Qy	866	CC	CTTAAGAAGAAAGCTATATCTCTGACACAGAAAGCCCTCTACAAACCTGAGACTC	925
Db	537	TC	CAAAAGAAAGAGCGCTATATTTCTGACACAGAGGCTCTCTGCAACACCTGGACTC	596
Qy	926	GG	CACTCCAGGCCCGCTGTCTCATGTATATCATGTACACAGCAGTGGAAATTTGGAA	985
Db	597	AG	CACTCCAGGCCCGCTGTCTCATGTATATCATGTATACAGCAGCAATGGAAATTTGGAA	656
Qy	986	TT	TGTGTTCAAATTCAGAGAGGCTTATCAAGAAACAGTGTTACATGATCAGATAATAGA	1045
Db	657	TT	TGTGTCTCAAAATTCAGAGGAACTTATACGAGACAGGTTACATGTATCAGATAATAGA	716
Qy	1046	AT	ATCTTTTACCCCTGTGTTGATTTTACACCTTTGGACTGCTCTGGCAAGGGCGAAATTT	1105
Db	717	AT	ACCTTTTACCCCTGTGTTATCATTTACACCTTTGGACTGCTCTGGGGAAGGGCGAAAGCT	776
Qy	1106	AC	AGTCTGGACAGCAATCCTCTAGGTAACCTCTTGGGCTGGCAAACTTCGACCC	1165
Db	777	AC	AGTCTGGGACAGCAATCCTCTAGGTAAGCTCTTTCAGGTGGCAAACTTTGACCC	836
Qy	1166	TT	TGGAATTTCTCGAGAGTTTAAAGAAATTAACATCAAGTGGACAGCTGGAGGAAAT	1235
Db	837	CT	TGGAATTTCTTGAAGAGTTTAAAGAAATTAACATCAAGTGGACAGCTGGAGGAAAT	896
Qy	1226	GC	TGATATAGCGTGTAGGTTGTGTATGTGTATATGAGACCCGCCCTGCTCATTCGGCGCGA	1285
Db	897	GC	TGATATTAAGCCGMAATTTGGCATGTGGTACATGTAGCCGGCTTGTCTTCAACCCAGCCGA	956
Qy	1286	TC	CAGACTGGCCCGCCACAGCCGCCCAAAAAATTCAAACCAAACTCTGTGATTTGGCCCT	1345
Db	957	CC	CAGATTTGCCCTGTCCACAGCCCTTAACAAAAATTCAAACCAAACTCTTGTATTTGGCCCT	1016
Qy	1346	TG	TTTTGGAATGTGATATGTCATGTGCTTATCCAGAAAGTATATGCACTGGCAGAGAGATT	1405
Db	1017	TG	TTTTGGAATGTGATATGTCATGATGCTTATCCAGGAAGTATATGCACTGGCAGAGAGATT	1076
Qy	1406	GA	TTTGTGGGTCAGCACTGCAAGAACAGACAGCTGGAAGAACTGTCAGCGGCCCATGCGCTCA	1465
Db	1077	GA	TTTGTGGGTCGTCACGTCAGAAATGTCCACTGGAAGAACTTTCAGCGCTCAGCGCCCTCA	1133
Qy	1466	GA	CCATTTTCCAGTTTAAATGACTCCCAAGCAAAATGTACAGGCACTTCAAGGGGTACGAGTA	1525
Db	1137	AA	CCATTTTCCAGTTTAAATGACTCCCAAGCAAAATGTATGAACACATTCAGGGGCTACGACTA	1196
Qy	1526	TG	TCTCACAACATCAACTGGAACAGGACAAAGCGGCAAGCATCTCTGGAGGCTGTGGCAAG	1588
Db	1197	TG	TCTCTTCACATCAACTGGAATGGAAGACAGGGCAGCCGCAATCTGTGGAGGCTGTGGCAAG	1255
Qy	1586	GAC	ATATGTGGAGGATGCTTCATCAGAGTGTGGCAGACAAATCCACTCAAAAGGCTCTTTC	1644
Db	1257	GAC	TTTACTGTGAGGATGCTTCATCAAAAGTGTGCCCCCAAAATCTCACTCAAAAGGCTCTTTC	1311

[illegible]

QY 1646 CTTACACCAACGACCCCTGGAGACATCCGTAATCTTCTGTGACGTGATGATCCG 1705
 Db 1317 CTTACACCAACGACCCCTGGAGACATCCGTAATCTTCTGTGATGATGATGATCCG 1376
 QY 1706 CGTGGCCAGGCGCTACTTACTACTGCTGCGCTATGCGCTGTACCAATGCTGCGTGGGA 1765
 Db 1377 AGTGGCCAGGCGCTACTTACTACTGCTGCGCTATGCGCTGTACCAATGCTGCGTGGGA 1436
 QY 1766 CTGCTCCAAATCCAGAGTGGCGCTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1825
 Db 1437 CTGCTCCAAATCCAGAGTGGCGCTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1496
 QY 1826 GCGTGGAGGACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885
 Db 1497 GCGTGGAGGACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
 QY 1886 GGTGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1945
 Db 1557 GGTGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1616
 QY 1946 CTTTACGTAACAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2005
 Db 1617 ATTACGTAACAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1676
 QY 2006 GAAGCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065
 Db 1677 CAAGCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
 QY 2066 GCGCGGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCT 2125
 Db 1737 GCGCGGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCGCT 1796
 QY 2126 GGTGTTCAATTTTGGCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185
 Db 1797 GGTGTTCAATTTTGGCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856
 QY 2186 TCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245
 Db 1857 CAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
 QY 2246 AGTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2305
 Db 1917 GGTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1976
 QY 2306 CCCAGCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365
 Db 1977 CCCAGCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036
 QY 2366 TGTCCAGCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2425
 Db 2037 CGTTCAGCTCCCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2096
 QY 2426 GCGCTCCAGAGTCTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2485
 Db 2097 ACGCTCTGAGTCTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2156
 QY 2486 CCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2545
 Db 2157 TCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2216
 QY 2546 CTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2605
 Db 2217 CTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2276
 QY 2606 TCTTCTCTCTGAAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2665
 Db 2277 TCTTCTCTCTGAAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2336
 QY 2666 GGGGGTCAAGCTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2725
 Db 2337 GGGGGTCAAGCTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2396

QY 2726 ACCTGGGAACACAGAGATATGACTTATTTGCTGACAAATTCAAATCTTTCTTTCTTA 2785
 Db 2397 TCCCGCGGAACACAGAGATATGACTTATTTGCTGACAAATTCAAATCTTTCTTTCTTA 2456
 QY 2786 CAACATGATATATAGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2845
 Db 2457 CAACATGATATATAGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2516
 QY 2846 CCTACAGAGAGTTCAGTACAGTGAAGTATGTCATGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2905
 Db 2517 CCTACAGAGAGTTCAGTACAGTGAAGTATGTCATGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2576
 QY 2906 CAAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2965
 Db 2577 CAAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2636
 QY 2966 TCACTGGGAACCGGGAATTCATGTCGCAAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3025
 Db 2637 TCACTGGGAACCGGGAATTCATGTCGCAAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2696
 QY 3026 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3085
 Db 2697 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2756
 QY 3086 GTTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3145
 Db 2757 GTTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2816
 QY 3146 CTTACGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3205
 Db 2817 CTTACGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2876
 QY 3206 CCGGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3265
 Db 2877 CCGGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2936
 QY 3266 GAGAAATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3325
 Db 2937 GAGAAATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2996
 QY 3326 GCGGAGACAGCTGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3385
 Db 2997 ACGAGACAGCTGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3056
 QY 3386 TACGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3445
 Db 3057 TACGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3116
 QY 3446 CATCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3505
 Db 3117 CATCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3176
 QY 3506 CGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3565
 Db 3177 AGTGTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3236
 QY 3566 GCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3625
 Db 3237 TCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3296
 QY 3626 GCGCGTGTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3685
 Db 3297 GCGCGTGTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3356
 QY 3686 TTTGGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3745
 Db 3357 TTTGGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3416
 QY 3746 CATGTTTGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3805
 Db 3417 CATGTTTGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3476
 QY 3806 GGGATCTGAGTTCAGCTTATGTCAGGTAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3865

QY	446	CGTGTCCCGGGAGAGGCCGCTGGAAGCGGAGAGCGCAGACGGAGCGGGGGCTGCGCGG	505
Db	120	CGGGGGCTTGGGGCAGGGCAGGGCGGGGGGGGGGGCGGACAGACCGGGGAGACCGACCG	179
QY	506	TGCTGCGCGCGGACCGGGAGCTATCTGCACCGGGCCAGCTCTCTCGAGCGCCGCTTGCG	565
Db	180	C - - - GCGCGCGGACCGGGAGCTATCTGCACCGGGCCAGCTCTCTCGAGCGCCGCTTGCG	236
QY	566	TCGTGAGCAGATTTTCCAAAGGGGAAGGCTACTGCGGAGAGCGCCTACTGTGCTGAGAC	625
Db	237	TCGTGAGCAGATTTTCCAAAGGGGAAGGCTACTGCGGAGAGCGCCTCTGTGCTGAGAC	296
QY	626	GAAGCTTCAGAGACTCTTATTTAAACGTGGTGTTCACATTCAAAAAAACCTGCGGCAAGTT	685
Db	297	GAAGTTTTCAGAGACTCTTATTTAAACGTGGTGTTCACATTCAAAAAAACCTGCGGCAAGTT	356
QY	686	CTTAGTGTGGGCTCCCTCATATTTGGGGGCTTGCGGGTGGATTTAAAGACGCAACT	745
Db	357	TTTGGTGTGGGCTCTCTCATATTTGGGGGCTTGCGGTGGATTTAAAGGCAAGCT	416
QY	746	CGAGACCAACGTGAGAGAGCTGTGGGTGGAAAGTTTGGAGAGCAGTAAAGTCTGCAATTTAA	805
Db	417	CGAGACCAACGTGAGAGAGCTGTGGGTGGAAAGTTTGGAGAGCAGTAAAGTCTGCAATTTAA	476
QY	806	TTATPACTCGCCAGAAAGTTGGAGAAAGGCTATGTTTAATCCTCACTCATGATATCAGAC	865
Db	477	TTATPACTCGCCAGAAAGTTGGAGAAAGGCTATGTTTAATCCTCACTCATGATATCAGAC	536
QY	866	CCCTAAAGAAGAAAGGTCTATGTGCTGACCAAGAAAGCGCTCTCTACAAACACTTGACTC	925
Db	537	TCCAAAAAGAAAGGCGCTATGTGCTGACCAAGAAAGCGCTCTCTCTGCAACACTTGACTC	596
QY	926	GGCAGCTCCAGGCGACCGGTGCAATGTATCATATCATATACAAACAGGAGTGAATTTGGACA	985
Db	597	AGCAGCTCCAGGCGACAGTGTGTGACGCGTCTCATGTATTAACAGGCAATGGAATTTGGAACA	656
QY	986	TTTTGTGTACAAATTCAGAGAAAGCTTTATCAGAGAAACAGGTTACATGATCAGATTAATAGA	1045
Db	657	TTTTGTGTACAAATTCAGAGAAAGCTTTATCAGAGAAACAGGTTACATGATCAGATTAATAGA	716
QY	1046	ATATCTTTTACCTTGTTTGTATTTATACCTTTGGAGCGCTTCGGGAAGGGGCGCAATT	1105
Db	717	ATATCTTTTACCTTGTTTGTATTTATACCTTTGGAGCGCTTCGGGAAGGGGCGCAAACT	776
QY	1106	ACAGCTTGGGACAGCATATCTCTAGGTAAACCTCTTTGGGCTGGACAAACTTTCAGACC	1165
Db	777	ACAGCTCGGGACAGCATATCTCTAGGTAAAGCTCTTTACGGTGGACAAACTTTCAGACC	836
QY	1166	TTTTGGATTCCTCGSAGAGAGTTAAAGAAATTAACATTCAAAGTGGACAGCTGGAGGAAT	1225
Db	837	CTTTGGAATTCCTCGSAGAGAGTTAAAGAAATTAACATTCAAAGTGGACAGCTGGAGGAAT	896
QY	1226	GCTGATAAAGGCTGAGGTTGGTATGATGGTTTCATGGAGACGCGCCGCTCATTCGGGCGGA	1285
Db	897	GCTGATAAAGGCGSAGGTTGGCATGGGTATCATGGAGCGCGCTTGGCTCAACCCAGCGGA	956
QY	1286	TCACAGACTCCCGCGCACAGGCCCCCAACAAAATTCACAAAACCTTGTATATGAGCCT	1345
Db	957	CCACAGATTCCTCCGCGCACAGGCCCTTAACAAAATTCACAAAACCTTGTATGAGCCT	1016
QY	1346	TGTTTTGAATGGGAGATGTGCATGGCTTATTCACAAAAGTATATGACATGCGACAGGAGATT	1405
Db	1017	TGTTTTGAATGGGAGATGTGCATGGCTTATTCACAAAAGTATATGATGCGACAGGAGATT	1076
QY	1406	GATGTGTGGGTGCACAGTCCAGAAACAGCACTGGAAAACTGTGCAGCGCCCATGCGCTGCA	1465
Db	1077	GATGTGTGGGTGTGACCGTCAAGAAATCCCACTGGAAAACTGTGACGCTTACGCGCTTCA	1136
QY	1466	GACCAATGTTCCAGTTAATACTCTCCACAGCAAAATGTACAGACACTTCAAGGGATACAGATA	1525
Db	1137	AACCAATGTTTCCAGTTAATACTCTCCCAAGCAAAATGTATGAACACTTCAAGGGGCTACAGCTA	1196
QY	1526	TCTCTCACACATCACTGGAAGAGACAAAGCGGACGCACTCTCTGAGAGCTGTGACAG	1585

Db	1197	TGTCTCTCACATCAACTGGAAATGAAGACAGGGCACCAGCATCTCGAGAGCCCTGGCAGAG	125
QY	1586	GACATATGTGGAGGTGGTTTCATCAAGAGTGTGCACAGAACTCACCTCAAAAGGTGCTTAC	164
Db	1257	GACTTACGTGAGAGGTGGTTTCATCAAAAGTGTGCCCCCAAACTCCACTCAAAAGGTGCTTC	131
QY	1646	CTTACACCACCCAGACACCCTGGAGACGACATCTCTGAATCTCTCTGACGTGACGTGATCCG	170
Db	1317	CTTACAAACAGACACCCTGGAGACGACATCTTAAATCTCTCTCTGTATGTACAGTGCATCCG	137
QY	1706	CGTGGCCAGCGGCTACTTACTCATGCTCGCCATCTCGTCAATCGTCAACATGCTCGCGGGA	176
Db	1377	AGTGGCCAGCGGCTACTTACTCATGCTCGCCATCTCGTCAATCGTCAACATGCTCGCGGGA	143
QY	1766	CTGTCTCAAGTCCCAAGGTGCCGTGGGGCTGGCTGGCGTCTGCTGTGGTGCACGTACGT	182
Db	1437	CTGTCTCAAGTCCCAAGGTGCCGTGGGGCTGGCTGGCGTCTGCTGTGGTGCACGTACGT	149
QY	1826	GGCGCCAGAGCTGGCGGCTGCTCATATGATGAGAAATTCCTTTAACGCTGCACAACTCA	188
Db	1497	GGCGCCAGAGTATGGGCTCTCTGCTCTTATGATGCAATTCCTTTAAATGCTGCACAACTCA	155
QY	1886	GGTTTTGCCATTTCTGCGCTCTTGGTGTGTGTGATGATGTTTTCTCTTGGCCACGAC	194
Db	1557	GGTTTTGCCATTTCTGCTCTTGGTGTGTGTGATGATGTTTTCTCTTGGCCACGAC	161
QY	1946	CTTACAGTAAACAGAGACAGATTAAGAATCCCTTTTGAAGACAGGACCAGGGAGTGCCT	200
Db	1617	ATTACAGTAAACAGAGACAGATTAAGAGATTCATTCATTCAGACAGAGCATGGGAGTGCCT	167
QY	2006	GAAGCGCACAGAGACCAGCGTGGCGCTCACGTGCATCAGCAATGTCACAGCCTTCTCAT	206
Db	1677	CAAGCGCACAGGAGCCAGCGTGGCGCTCACGTGCATCAGCAATGTCACAGCCTTCTCAT	173
QY	2066	GGCGCGGTATATCCCAATTCGCCCTCTGGCGGGCTTCTCCTCCAGCGAGCGGTAGTAGT	212
Db	1737	GGCGCGGTATATCCCAATTCGCCCTCTGGCGGGCTTCTCCTCCAGCGAGCGGTAGTAGT	179
QY	2126	GGTGTTCATATTTGGCATATGTTGTGCTGCATTTTCTCGCATTTCTCGACATGATGATTTTA	218
Db	1797	GGTATTCATATTTTGGCATATGTTGTGCTGCATTTTCTCGCATTTTCTCGACATGATTTTA	185
QY	2186	TGCACGCGAGAGACGAGACTGGATATTTTCTGCTGTTTTTCAAGCCGCTTCGTACAGAG	224
Db	1857	CACACGTGAGACAGAAAGATTGGATTTTCTGCTGTTTTCAAGCCGCTTCGTACAGAG	191
QY	2246	AGGATTTACAGTTGGAACCTTAGGCTTCACCGACACACAGACATACATACCCGCTACAGCC	230
Db	1917	GGGATTTACAGTTGGAACCTTAGGCTTCACACAGACCTTCACAGTAACACCCGCTACAGCC	197
QY	2306	CCGACCTCCCTACAGACGCCACAGCTTTGCCATGAAGCGAGATTTACATGACAGTCCAC	236
Db	1977	CCGACCTCCCTACAGACGCCACAGCTTTGCCATGAAGCGAGATTTACATGACAGTCCAC	203
QY	2366	TGTCCAGCTTCGCGAGAGTAGACACCCCAACAGCAGTGTACTACACACACCGCTGAGCC	242
Db	2037	CGTTCAGCTTCGCGAGAGTAGATATACCTTCACAGCAGTGTACTACACACACCGCGGAGCC	209
QY	2426	GGCGTTCGAGATCTCTGTGAGCCCGTACCGTGCACGTGACACAGACACCTTCAGCTCCAGAG	248
Db	2097	ACGCTCTGAGATCTCTGTGAGCCCTGTGTACCGTACCCAGACAGACCTTCAGCTTCAGAG	215
QY	2486	CCGAGAGACACACAGTCCACAAAGGACCTGCTCTCCCAATTTCTCGAGTCCAGCCTCA	254
Db	2157	TCCCGAGACACACAGTCTTACCAAGGACCCGCTCTCCCAATTTCTCAGACCTCAGCCTCA	221
QY	2546	CTGCGTTCGAGCCCTCTGACGAAGTGGACACTCTCATCTTTTGGACGAGAAGCACTATGC	260
Db	2217	CTGCGTTCGAGCCCTCTGACGAAGTGGACACTCTCTGCTTTGACGAGAAGCACTATGC	227
QY	2606	TGCTTTCTCTTTGAAAACCAAAGCCAGGTAAGTGTGATCTCTCTTTTCTGGGCGTTGCT	265

Db 2277 TCCTTCCCTCCGAAACCCAAAGGCTGTAATCCCTTCTTCCGCGGCTTGC 2336
Qy 2666 GGGGGTCACCCCTTTATGGACCAACCGAGTGAAGAGCGGCTGGACCTTAACGACATGT 2755
Db 2337 GGGGGTCACCCCTTTATGGACCAACCGAGTGAAGAGCGGCTGGACCTTAACGACATGT 2396
Qy 2726 ACCTGGGGAAACCAAGAAATATGACTTTATGCTGCACATTCGAAATACCTTTCTTCTA 2785
Db 2397 TCCCGGGAAACCAAGAAATATGACTTTATGCTGCACATTCGAAATACCTTTCTTCTA 2456
Qy 2786 CAACATGATATATGATCACCAGAAAGAGACTACCCGAATATCCAGCACTTACTTTACGA 2845
Db 2457 CAACATGATATATGATCACCAGAAAGAGACTACCCGAATATCCAGCACTTACTTTACGA 2516
Qy 2846 CCTACACAGAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2905
Db 2517 CCTTCAAGAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2576
Qy 2906 CAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2965
Db 2577 CCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2636
Qy 2966 TGACTGGGAAACCTGGGAGATTCGCCAAACATTTAAAAATGATGATGATGATGATGATG 3025
Db 2637 TGACTGGGAAACCTGGGAGATTCGCCAAACATTTAAAAATGATGATGATGATGATGATG 2696
Qy 3026 CCTTGGCTTACAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3085
Db 2697 CCTTGGCTTACAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2756
Qy 3086 GTTGAATTAACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3145
Db 2757 GTTGAATTAACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2816
Qy 3146 CTACTGACGCGCTTGGGTGACAAAGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3205
Db 2817 CTACTGACGCGCTTGGGTGACAAAGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2876
Qy 3206 CCGGCGACACCGACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3265
Db 2877 CCGGCGACACCGACCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2936
Qy 3266 GAGAATTCGCGGACGAGAGCCCATGATGATGATGATGATGATGATGATGATGATGATGATG 3325
Db 2937 GAGAATTCGCGGACGAGAGCCCATGATGATGATGATGATGATGATGATGATGATGATGATG 2996
Qy 3326 GCGGAGACCTCAGACTTTTGTGAGGCAATTAAGAAATGAGGACATCTGACGACATA 3385
Db 2997 ACAGAGACCTCAGACTTTTGTGAGGCAATTAAGAAATGAGGACATCTGACGACATA 3056
Qy 3386 TAGAGGCTGGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3445
Db 3057 TAGAGGCTGGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3116
Qy 3446 CATTGAGCTGCGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3505
Db 3117 CATTGAGCTGCGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3176
Qy 3506 CGTGTGCGGTCTTCTTCTTCTGAAACCCCTGAGAGCGCGGATCATTTGATGATGCTGCTG 3565
Db 3177 AGTGTGCGGTCTTCTTCTTCTGAAACCCCTGAGAGCGCGGATCATTTGATGATGCTGCTG 3236
Qy 3566 GCTGATGACGCTGAGCTGCTGCGGATGATGAGGCTCATCGGAATCAAGCTAGAGCGCT 3625
Db 3237 TCTGATGACGCTGAGCTGCTTGGCATGATGAGGCTCATTTGGGATCAAGCTAGAGCTGCT 3296
Qy 3626 GCGCGGTGATCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3685
Db 3297 GCGCGGTGATCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3356
Qy 3686 TTTGGCTTTTGAAGGCTGAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3745
Db 3357 TTTGGCTTTTGAAGGCTGAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3416

Qy 3746 CATGTTGACACCGCTGCTGATGAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3805
Db 3417 CATGTTGCTCCGCTTGTGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3476
Qy 3806 GGGATCTAGATTGCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3865
Db 3477 AGGTCGGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3536
Qy 3866 CCTGCGCTTCTCAATGGGCTGCTTGGCTTCCCGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 3925
Db 3537 CTGGGGGGTTCATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3596
Qy 3926 TCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3985
Db 3597 TCCTAGGTGCTTCCAGGCAATGCTTAAACCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3656
Qy 3986 CCCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4045
Db 3657 TCCTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3716
Qy 4046 CGACTCGGAGTATGATTCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4105
Db 3717 CGACTCGGAGTATGATTCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3776
Qy 4106 CGAGGCCGACAGGCGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4165
Db 3777 CGAGGCCGACAGGCGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3836
Qy 4166 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4225
Db 3837 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3896
Qy 4226 CCGGAGACAGAGCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4285
Db 3897 CCGGAGACAGAGCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3956
Qy 4286 GCCCGGACAGAGCGCCCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4345
Db 3957 GCCCGGAGAGGATCCCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4016
Qy 4346 CCGTTTTGAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4405
Db 4017 CCGTTTTGAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4076
Qy 4406 TCGCGGGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4465
Db 4077 CCGTGGGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4136
Qy 4466 GCCCGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4525
Db 4137 GCCCGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4196
Qy 4526 GCACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4581
Db 4197 GCATCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4250
Qy 4582 -----GCTACCTGAGACTGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4636
Db 4251 TCGAGCTACCTGAGACTGATCAGCGGGATTTATGAGAGATTCATGAGCTTTCTGCTGCTGCTG 4310
Qy 4637 CCGGTGAGAGAGGATTCGAAGGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4696
Db 4311 CAGGTGAGAGAGGAGACTCAAGAGGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4370
Qy 4697 GAGAGAGCGCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4756
Db 4371 GAGAGAGCGCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4430
Qy 4757 AAAGATTGAAACCGCCGACCTCTTCTGAGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 4816
Db 4431 AAAGATTGAAACCGCCGACCTCTTCTGAGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 4489

QY 4817 AGTATGAAAGATGCCCTGTCAGACAGAGATTCATTGTTACTGTAAACCATTTGTA 4876
 Db 4490 AATTATG-----GGAGGCAAGTTCATTGTTACTGTAACTGATTTGTA 4530
 QY 4877 TATTTTGTAAATATTTCTATATAATTTAAGAGATGTACACATGTTATATAGAGAG 4936
 Db 4531 TATTTTGTAAATATTTCTATATAATTTAAGAGATGTACACATGTTATATAGAGAG 4936
 QY 4937 GAGAGATGTAAAGTGTATGATCTGGGGCTTTCACACTCTGCCCCAGAGTGTGAGGCC 4996
 Db 4589 AATGCTGTACAGT-CTATTTCTGGGGCTTTCACACTCTGCCCCAGAGTGTGAGGCC 4647
 QY 4997 ACAGTGGGCTCTCCGTTATTTGATGTGGGCTCCGTCGACACACCAAGCTTATAGT 5056
 Db 4648 ACA--GGGGCCCTTCCCTGCTGATGTTGCTCTGTCGACCAACCAACCTTAACTTAG 4705
 QY 5057 CTAA--TTTCAGCATATGTTGCTGCTGCTTAAATATTTGATATTTACTTGT 5108
 Db 4706 TTTTAAAAAAATCTCCAGCATATGCTGCTGCTTAAATATTTGATATTTACTTGT 4765
 QY 5109 ATATTTTATGCAAAATTTGCTTATGTAATAGATTTATTTGTAAGGTTCTGTTAAA 5168
 Db 4766 ATATTTTATGCAAAATTTGCTTATGTAATAGATTTATTTGTAAGGTTCTGTTAAA 4824
 QY 5169 ATATTTTATGCTATACACACACCTGTGTAGTATGAAATGTTACTGTTAACTTTCA 5228
 Db 4825 ATATTTTATGCTATACACACCTGTGTAGTATGAAATGTTACTGTTAACTTTTG 4884
 QY 5229 AACAGCTATGCGTGAATTTTGTGTTAATGACAGATGTAAGAGGC 5280
 Db 4885 AACAGCTATGCGTGAATTTTGTGTTAATGACAGATGTAAGAGGC 4931

RESULT 9
 US-08-954-701A-3
 : Sequence 3, Application us/08954701A
 : GENERAL INFORMATION:
 : APPLICANT: SCOTT, MATHEW P
 : APPLICANT: GOODRICH, LISA V
 : APPLICANT: JOHNSON, RONALD L
 : TITLE OF INVENTION: Patched Genes and their use
 : NUMBER OF SEQUENCES: 19
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley, Hoag & Eliot
 : STREET: One Post Office Square
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: ASCII(text)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/954,701A
 : FILING DATE: 20-OCT-1997
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Vincent, Matthew P.
 : REGISTRATION NUMBER: 36709
 : REFERENCE/DOCKET NUMBER: SUV-003.08
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-832-1000
 : TELEFAX: 617-832-7000
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5187 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US-08-954-701A-3

Query Match 71.9%; Score 3801.2; DB 13; Length 5187;
 Best Local Similarity 88.1%; Pred No. 0;
 Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

QY 446 CGGTGCCCCGAGCGCCGCTGAGAGCCGGAGAGCCAGACGAGCCGCGGCGCG 505
 Db 120 CGGGCCCTGGGAGGAGGAGCGCCGCGGAGAGGCGACAGCGAGCGGAGCGGACCG 179
 QY 506 TGCTGCCCGCGCGAGACCGGAGACTATGTCACCGGCCACCTACTGCGAGCGCCCTTGGC 565
 Db 180 C---GCCGCGCGGAGCGGAGACTATGTCACCGGCCACCTACTGCGAGCGCCCTTGGC 236
 QY 566 TCTGAGCAGATTTTCCAAAGGAGGCTACTGCGCGGAAAGCGCCACTGCGGTGAGAGC 625
 Db 237 TCTGAGCAGATTTTCCAAAGGAGGCTACTGCGCGGAAAGCGCCACTGCGGTGAGAGC 296
 QY 626 GAAATTTGAGAGACTCTTATTTAACTGGGTTGTTACATTTCAAAAACCTGCGCAAGTT 685
 Db 297 GAAATTTGAGAGACTCTTATTTAACTGGGTTGTTACATTTCAAAAACCTGCGCAAGTT 356
 QY 686 CTGCTGTGTGGGCTCTCATATTTGGGCGCTTCCGCGTGAGATTAAAGCAGCAACT 745
 Db 357 TTTGGTGTGGGCTCTCATATTTGGGCGCTTCCGCTGCGGATTAAAGCAGCAACT 416
 QY 746 CGAGACCAACGTTGAGAGAGCTGTGGGTTGAGAGGAGCAGTAAAGTGAATTTAA 805
 Db 417 CGAGACCAACGTTGAGAGAGCTGTGGGTTGAGAGGAGTGAAGTGAATTTAA 476
 QY 806 TTTATCTGCGCAAGATTTGAGAGAGCTATGTTTAACTCTCACTCATGTATACAGAC 865
 Db 477 TTTATCTGCGCAAGATTTGAGAGAGCTATGTTTAACTCTCACTCATGTATACAGAC 536
 QY 866 CCGTAAAGAAAGAGTGTCTATATCTCTGACCAAGAGCGCTCTCTCAACCTGAGCTC 925
 Db 537 TCCAAAGAAAGAGGCGCTTAAATGTTCTGACCAAGAGCGCTCTCTCAACCTGAGCTC 596
 QY 926 GGCACCTCCAGGCGACCGCTGCTCATGTATACATGTACACAGGAGCTGGAATTTGGAACA 985
 Db 597 AGCACTCCAGGCGACGCTGCTCATGTATACATGTATACAGGAGCTGGAATTTGGAACA 656
 QY 986 TTTGTGTACAAATCAGAGAGACTTATACACAGAAACAGTTACATGATCAGATATAGA 1045
 Db 657 TTTGTGTACAAATCAGAGAGACTTATACACAGAAACAGTTACATGATCAGATATAGA 716
 QY 1046 ATATCTTACCCCTGTTGATTTATATACACCTTTGAGACGCTCTCTGGAAGGGCGCAAT 1105
 Db 717 ATATCTTACCCCTGTTGATTTATATACACCTTTGAGACGCTCTCTGGAAGGGCGCAAT 776
 QY 1106 ACAGTCTGGAGACGATACCTCTAGTAAACCTCTTGGCGTGAACAACCTGAGCC 1165
 Db 777 ACAGTCTGGAGACGATACCTCTAGTAAACCTCTTGGCGTGAACAACCTGAGCC 836
 QY 1166 TTTGGAATTTCTGGAAGATTAAGAAAAATAAATACTATCAAGTGAACGCTGGAGAGAA 1225
 Db 837 CTGGAATTTCTGGAAGATTAAGAAAAATAAATACTATCAAGTGAACGCTGGAGAGAA 896
 QY 1226 GCTGAATTAAGGCTGAGGTTGTCATGTTACATGTAAGAGCGCCCTGCTTAATCCGCGCA 1285
 Db 897 GCTGAATTAAGGCTGAGGTTGTCATGTTACATGTAAGAGCGCCCTGCTTAATCCGCGCA 956
 QY 1286 TCCAGACTGCGCCGCGACAGCCCGCCCAAAAATTAACAACAACCTGATATGAGCCCT 1345
 Db 957 CCGAGATTTGCGCTGCGACAGCCCGCCCAAAAATTAACAACAACCTGATATGAGCCCT 1016
 QY 1346 TGTTTGAGTGTGATGTCATGCTTATCCAGAAATATATGACTGCGAGAGAGTT 1405
 Db 1017 TGTTTGAGTGTGATGTCATGCTTATCCAGAAATATATGACTGCGAGAGAGTT 1076
 QY 1406 GATTGTGGGTGCGACAGTCAAGACAGACTGGAACAACTGTCAGAGCCGCTCATGCTGCA 1465
 Db 1077 GATTGTGGGTGCGACAGTCAAGAAATGCGACTGGAACAACTGTCAGAGCCGCTCATGCTGCA 1136

Oy	1466	GACATGTTCCAGTTAAATGACATCCCAAGCAAAATGTCAGAGACCTTCAAGGGGTACAGGTA	1525
Db	1137	AACCATGTTCCAGTTAAATGACATCCCAAGCAAAATGTAATGACATTTCAAGGGGTACAGGTA	1196
Oy	1526	TGTCACACATCAACTGGAAAGGAGACAAGCGGCGACCATCTTGAGGGCTTGGCAGAG	1585
Db	1197	TGTCACATCAACTGGAAATGAAAGAGGAGCGGCGACCATCTTGAGGGCTTGGCAGAG	1256
Oy	1586	GACATATGTGGAGGTGGTTCAATCAGAGTGTCCGACAGAACTCCACTCAAAAGGTGCTTTC	1645
Db	1257	GACATACGTGGAGGTGGTTCAATCAAAAGTGTGGCCCCCAAACTCCACTCAAAAGGTGCTTTC	1316
Oy	1646	CTTTCACCAACAGACCCCTGGAGGACATTCCTGAAATCTTTCTGACGTACGTGCATCCG	1705
Db	1317	CTTCACCAACAGACCCCTGGAGGACATCTTAATCTCTTGATGTAGTGTGCATCCG	1376
Oy	1706	CGTGGCCAGCGGCTACTTACTCATGCTCGCTATGCTCTGTAAACATGCTGGCGTGGGA	1765
Db	1377	AGTGGCCAGCGGCTACTCTACATGCTGTGCTATGCTCTGTTTAAACATGCTGGCGTGGGA	1436
Oy	1766	CTGCTCCAAAGTCCCAAGGGTGGCGGTGGGCGGTGGCTGGCGTCTGCTGGTTGCATGTAGT	1825
Db	1437	CTGCTCCAAAGTCCCAAGGGTGGCGGTGGGCGGTGGCTGGCGTCTGTTGGTTGCGCTGTAGT	1496
Oy	1826	GGCTGCAGACATGGGGCTGTGGCTATGATCGGAATTTTCCTTTAAACGTTGCACAACTCA	1885
Db	1497	GGCTGCAGGATTTGGGGCTGTGGCTTGTGATTTGGCATTTTCTTTTAAATCTGCAGCACTCA	1556
Oy	1886	GGTTTTGCCATTTCTTCGCTCTTGTTGGTGTGGTATGATGTTTTTCTTTGGCCCCACGC	1945
Db	1557	GGTTTTGCCGTTTTCTTGGCTTGGTGTGGTATGATGTTTTTCTTCTTGGCCCCATGC	1616
Oy	1946	CTTCAGTGAACAGACACAATTAAGAATCCCTTTTGAGAGACAGACCGGGAGTGCCT	2005
Db	1617	ATTCACTGAAACAGAGACAATTAAGAGATTCATTTTGAGAGACAGACATGGGAGTGCCT	1676
Oy	2006	GAAGCGCACAGAGACCAGCGTGCGCTCACGTTCATCAGCAATGTCAAGCCCTTCTTCAT	2065
Db	1677	CAAGCGCACAGGAGCGCAGGTGGCGCTCACGTTCATCAGCAATGTCAAGCCCTTCTTCAT	1736
Oy	2066	GGCGGGTTAAATCCCAATTTCCGCTCTGGGGGGGTTTCCCTCCAGGACAGCGGATAGAT	2125
Db	1737	GGCGCGCATTTGATTCCTATTCCTCTGCTCCCTCGCAGCGGTTTCCCTCCAGGCTGCTGTGGTGT	1796
Oy	2126	GGTGTTCATTTTGGCCATGGTTCTGCTCATTTTCTGTGCATTTCTCGATGTGATTTATA	2185
Db	1797	GGTATTCATTTTGGTATGGTTCTGCTCATTTTCTGTGCATTTCTCGATGTGATTTATA	1856
Oy	2186	TTCAGCCGAGACAGGAGAGCTGATATTTTCTGCTGTTTACAAGCCCGCGACACAG	2245
Db	1857	CAGAGCTGAGGACAGAAAGTTGGATATTTTCTGCTGTTTACAAGCCCGCTGTGTACAGAG	1916
Oy	2246	AGTGTATTCAGTTTGAACCTTCAGGCTTCACACGACACAGACATACCCGCTACAGCCC	2305
Db	1917	GGTATTCAGTTTGAAGCTTCAGGCTTCACACAGAGCGCTACACAGATTAACACCCGCTACAGCCC	1976
Oy	2306	CCCACCTCCCTACAGACGCACACAGCTTTGGCCATGAAGCGCAATTTACATGCAGTGCAC	2355
Db	1977	CCCACCCCTACACAGGCACACAGCTTTGGCCACGAAGAACCATATTCATATGCAGTGCAC	2036
Oy	2366	TTCACAGCTTCGCGACGAGTACACACCCCAACAGCAAGTGTACATACCAACCGCTGAGGC	2425
Db	2037	CGTTACAGCTTCGCGACAGATATACCCCTCACAGCAAGTGTACTACACCAACCGCGCAGGC	2096
Oy	2426	GGCGTCCGAGATCTGTGTGACGCCCTCACCGTACACAGAGACCCCTCAAGCTGCAGAG	2485
Db	2097	ACGCTCTGAGATCTGTGTACAGCCTGTATACCGTACACCAAGCAACCTCAAGCTGCAGAG	2156
Oy	2486	CCCAAGACACACAGCTTCACAAAGGAGACCGGCTCCCAATTCCTCGAGATCCACCTTCA	2545
Db	2157	TCCCGAGACACACAGCTTCACAGGGAGCGGCTCTCCCAATTTCTCAAGTCCACCTTCA	2216

QY	2546	CTCCGCGAGGCCCCCTGTACGAGTGGAGACACTCTCATCTATCTGCTGGTGGAGAGACATATGC	2605
Db	2217	CTGCCTCGAGCCCCCTCGACCAAGTGGACACTCTCTCTCTTCTTGCAAGAGACATATGC	2276
QY	2606	TCCTTTCCTCTTGAAACCAAAGGCCAAGGTAGTGGATCTTCCTTTCTGGGCTTGC	2665
Db	2277	TCCTTTTCCTCTTGAAACCAAAGGCCAAGGTAGTGGATCTTCCTTTCTGGGCTTGC	2336
QY	2666	GGGGGCTCAGCCTTTATGGCACCAACCCGAGTGGAGAGACGGGCTGGACCTTACGGACATGT	2725
Db	2337	GGGGGCTCAGCCTTTATGGGACCAACCCGAGTGGAGAGACGGGCTGGACCTCAGGACATGT	2396
QY	2726	ACCTCGGGAACACAGAAATATGACTTTATTTGCTGCACAAATTAATCTTTCTTTCTTA	2785
Db	2397	TCGCCGGGAACCAAGAAATATGACTTCAATAGCTGGCCAACTTCAAGTACTTCTTTCTTA	2456
QY	2786	CACACATGTATATAGTACCCAGAAAGACATAACCCGAATATCCAGCATTTACTTTACGA	2845
Db	2457	CACACATGTATATAGTACCCAGAAAGACACTCCCGAAATATCCAGCACTTACTTTACGA	2516
QY	2846	CCTACACAGAGATTTAGTAAAGCTGAAGTATGATCATTTGGAGAAACCAACAGCTTCC	2905
Db	2517	CCTTCAATAGAGTTTACGCAATGTGAAGTATGTCTATCTGAGSAGAACAAAGCACTTCC	2576
QY	2906	CAAAATGTGGCTTCAGCTACTTTCAGAGACTTCGCTTCAGGGACTTCAGAGTCAATTTGACAG	2965
Db	2577	CCAAATGTGGCTTCAGCTACTTTCAGAGACTTCGCTTCAGGGACTTCAGAGTCAATTTGACAG	2636
QY	2966	TCACGTGGGAAACCGGGAAATATCATGTGCCAATTTACAAATATGATACATGAGTGAAGT	3025
Db	2637	TCACGTGGGAAACCTGGGAGGATCATGCCAAACATTTATAAAATATGATCAATATGACGGGGT	2696
QY	3026	CCTTGGCTTCAAACCTCTGTGTGCMAACCGGACACCGGAGTAAGGCCATTCACATCAACCA	3085
Db	2697	CCTCGCTTAAACCTCTGTGTGCAGACTGGCAGCGGAGCAAGGCCATTCACATTAATGCA	2756
QY	3086	GTTGACTAAACAGCGTCTGTGGATGCAGATGGCATCATTTAATTCACAGCGCTTTCTACAT	3145
Db	2757	GTTGACTAAACAGCGTCTGTGTAGCAGCATAGTGGCATCATTTAATTCGAGCGCTTTCTACAT	2816
QY	3146	CTTACCTGAGGGCTTGGGTGACGCAAGACGCCGTCGCTATGTGTCGCCGCCAGGCAACAT	3205
Db	2817	CTTACCTGAGCCGCTTGGGTGACGCAAGCAACCCCTGTATAGCTTACGCTGCTCCAGCGCAACAT	2876
QY	3206	CCGGCCACACCGACAGATGGGTCCACGACAAAGCCGCACTACATGCTCTGTAACAGGCT	3265
Db	2877	CCGGCCCTCACCGGCCGAGTGGGTCCATGTACAAAGCCGCACTACATGCGACAGACAGGCT	2936
QY	3266	GAGAAATCCCGGGGACGAGAGCCCATGACGTAATGGCCACTTCCTTCATACCAACGGGGT	3325
Db	2937	GAGAAATCCCAAGCAGAGAGCCCATGAGTACGCTCAAGTCCCTTTCTTACTCAACGGGCT	2996
QY	3326	GGGGGACACCTTCAGCTTTGTGAGAGGCATTTGAAAAGTAAGAACCATCTGCACAACTA	3385
Db	2997	ACGAGACACCTTCAGACTTTGTGAAAGCATAGAAAAGTGAAGTCACTCTGTACAACCTA	3056
QY	3386	TACGAGCCTGGGGCTCTCCAGTATACCCCAAGCGGTACCCCTCTCTCTTGGGGAGGACTA	3445
Db	3057	TACGAGCCTGGGACTGTCCAGTATACCCCAATGGCTTACCCCTCTCTGTCTGGGGACATA	3116
QY	3446	CATCGGCTCCCGCAGCTGGCTGCTGCTTTCATTCAGCGTGGTGTGGCTTCGACACTTCT	3505
Db	3117	CATCAGCCTGGCGCCTACTGGCTGCTGCTATCCTATCAGCGTGGTGGCTTCGACAGTTTCT	3176
QY	3506	CGTGTGCGCTTCTTCTCTTTGTGAACCCCTTGAAGGGCCGGGATCATTTGTATGGTCCCTGGC	3555
Db	3177	AGTGTGCGCAGTCTTCTCTCTTGAACCCCTTGAAGGGCCGGGATCATTTGTATGGTCCCTGGC	3236
QY	3566	GCTATGACGCGTGGAGTGTTCGGCATGATGGGCGCTCATGGAAATCAAGCTCACTGGCGGT	3625
Db	3237	TCGTGATGACCGTGGAGCTCTTTTGGCATGATGGGCGCTCATTTGGGATCAAGCTGAGTGGCTGT	3286
QY	3626	GCCCGTGGTATCATCTGATCGCTTCTGTGGCATATAGAGTGAATTCACCGTTACGTTTC	3685

: LENGTH: 5187 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: CDNA
 : US-08-954-701a-9

Query Match 71.9%; Score 3801.2; DB 13; Length 5187;
 Best Local Similarity 88.1%; Pred. No. 0;
 Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11:

QY 446 CGTCCGCCGCGGACGCGGCTGAGGCGGAGCGCGACAGCGGCGGCGCGG 505
 DB 120 CGGGGCCCTGGGCGAGGCGCGCGCGGAGCGCGACAGCGCGGAGCGCGACCG 179
 QY 506 TGTGCGCGCGCGGCGGAGGATCTGACGCGCGCGCGCGCGCGCGCGCGCG 555
 DB 180 C--GCGCGCGCGGACGCGGAGCTATCTGACGCGCGCGCGCGCGCGCGCGCG 236
 QY 566 TCTGAGAGAGATTTCCAGAGGAGAGGCTACTGGCGGAGAGCGCGCGCTGAGAG 625
 DB 237 TCTGAGAGAGATTTCCAGAGGAGAGGCTACTGGCGGAGAGCGCGCGCTGAGAG 296
 QY 626 GAAGTTTCAGAGAGCTTTATTTAACTGGCTTTTACATTCAAAAAACTGCGCAAG 685
 DB 297 GAAGTTTCAGAGAGCTTTATTTAACTGGCTTTTACATTCAAAAAACTGCGCAAG 356
 QY 686 CTGGGTTGGGCGCTCCATATTTGGGCGCTTCGCGGCGGAGTTAAAGCGCGCAAC 745
 DB 357 TTTGGTTGGGCTCTCTCATATTTGGGCGCTTCGCGGCGGAGTTAAAGCGCGCAAC 416
 QY 746 CGAGACCAAGCTGAGAGAGCTGTGGTGGAGTTGGAGAGAGAGTAACTGTAATTA 805
 DB 417 CGAGACCAAGCTGAGAGAGCTGTGGTGGAGTTGGTGGAGAGAGTAACTGTAATTA 476
 QY 806 TTATATCTGCCAGAGATTTGAGAGAGAGCTATGTTTAACTCCTCACTGATACAG 865
 DB 477 TTATATCTGCCAGAGATTTGAGAGAGAGCTATGTTTAACTCCTCACTGATACAG 536
 QY 866 CCTTAAGAGAGAGTGTATATGTCTGACAGAGAGGCGCTCAACACCTGAGAC 925
 DB 537 TCCTAAGAGAGAGGCGCTATATGTCTGACAGAGGCGCTCTCTCAACACCTGAGAC 596
 QY 926 GGCATCCAGGCGAGCGCTGTCTCATATGATATGATACAGAGGCGAGTAACTGAG 985
 DB 597 AGCATCCAGGCGAGCTGTCTCATATGATATGATACAGAGGCGAGTAACTGAG 656
 QY 986 TTTGTGTTACAAATCAGAGAGAGCTTATCAGAGAGAGGTTACATGATACAGTAA 1045
 DB 657 TTTGTGTTACAAATCAGAGAGAGCTTATCAGAGAGAGGTTACATGATACAGTAA 716
 QY 1046 ATATCTTACCTTTGTTGATATATACACCTTGGACGCTCTCTGGAAGGCGGAAAT 1105
 DB 717 ATATCTTACCTTTGTTGATATATACACCTTGGACGCTCTCTGGAAGGCGGAAAT 776
 QY 1106 ACACTCTGGAGAGAGATCTCTAGTAAACCTCTTGGCGTGGAGCAAACTTCAGCC 1165
 DB 777 ACAGTCCGAGAGAGATCTCTAGTAAACCTCTTGGCGTGGAGCAAACTTCAGCC 836
 QY 1166 TTTTGGAGATTTCTGGAAGAGTTAAAGAAAATTAACATATCAGTGGAGAGTAA 1225
 DB 837 CTTGGAATTTCTGGAAGAGTTAAAGAAAATTAACATATCAGTGGAGAGTAA 896
 QY 1226 GCTGAATTAAGGCTGAATGTTGATGATATACATGAGCGCGCGCTGCTCAATCCGCG 1285
 DB 897 GCTGAATTAAGGCTGAATGTTGATGATATACATGAGCGCGCGCTGCTCAATCCGCG 956
 QY 1286 TCCAGACTCCCGCGCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1345
 DB 957 CCGAGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1016
 QY 1346 TGTTTTGAATGTTGATGATGCTCATGCTTATCCAGAAAGTATATGACATGCGCAG 1405

DB 1017 TGTTTTGAATGTTGATGATGCTCATGAGGTTTATCCAGAGATATATGCAATGGCAGAGAG 1076
 QY 1406 GATTGTGGGAGGCGAGCTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1465
 DB 1077 GATTGTGGGAGGCGAGCTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
 QY 1466 GACCATGTTCCAGTTAAATGATGATCCCAAGCAATATGACAGAGAGAGAGAGAGAG 1525
 DB 1137 AACCATGTTCCAGTTAAATGATGATCCCAAGCAATATGATGATGATGATGATGATGAT 1196
 QY 1526 TGTCTACACATTCACATCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1585
 DB 1197 TGTCTACACATTCACATCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256
 QY 1586 GACATATGTTGAGAGGTTGTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1645
 DB 1257 GACTTACGTTGAGAGGTTGTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1316
 QY 1646 CTTCACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1705
 DB 1317 CTTCACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1376
 QY 1706 CGTGGCCAGCGGCTACTTACTCATGCTGCGCTATGCTGCTAACCATGCTGCGTGG 1765
 DB 1377 AGTGGCCAGCGGCTACTTACTCATGCTGCGCTATGCTGCTAACCATGCTGCGTGG 1436
 QY 1766 CTGCTCCAGAGTCCAGAGGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1825
 DB 1437 CTGCTCCAGAGTCCAGAGGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1496
 QY 1826 GGCCTGACAGAGTGGGCGCTGCTCATGATGATGATGATGATGATGATGATGATGAT 1885
 DB 1497 GGCCTGACAGATTTGGGCGCTGCTCATGATGATGATGATGATGATGATGATGATGAT 1556
 QY 1886 GGTTTTGCATTTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1945
 DB 1557 GGTTTTGCATTTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1616
 QY 1946 CTTGACGTAAGACAGAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTA 2005
 DB 1617 ATTGACGTAAGACAGAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTA 1676
 QY 2006 GAAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065
 DB 1677 CAAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
 QY 2066 GGCCTGACATTTTCCATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125
 DB 1737 GGCCTGACATTTTCCATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
 QY 2126 GGTGTTCAATTTTCCATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185
 DB 1797 GGTGTTCAATTTTCCATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856
 QY 2186 TCGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245
 DB 1857 CAGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
 QY 2246 AGTATTCAGAGTTAAGCTCAGGCTACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 2305
 DB 1917 GGTGATTCAAGTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976
 QY 2306 CCGACCTCCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365
 DB 1977 CCGACCTCCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036
 QY 2366 TGTTCACAGTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2425
 DB 2037 CGTTACAGTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2096
 QY 2426 GCGCTCCGAGAGATCTCTGTCAGAGCGCGCTACCGGTACAGAGAGAGAGAGAGAGAG 2485

Db 2097 ACCGCTGAGATCTCTGTACAGCCTGTTACCGTCAACCCAGCAACCTCAGCTGTGAGAG 2156
 Qy 2486 CCCAGAGAGACACGACTCCACAGAGGAGCCTGCTCCAGTGTCTCCGACTCCAGCTCCA 2545
 Db 2157 TCCGAGAGAGACACGACTCCACAGAGGAGCCTGCTCCAGTGTCTCCGACTCCAGCTCCA 2216
 Qy 2546 CTGCTCTGAGCCCCCTGTACGAAGTGACACTCTCATCTTTTGTGAGAGCAGTATGC 2605
 Db 2217 CTGCTCTGAGCCCCCTGTACGAAGTGACACTCTCTCTGTTGAGAGAGCAGTATGC 2276
 Qy 2606 TCTTTTCTGTGAACCAAAAGCAAGTATGCTGATCTCTCTCTTTCTGGGGCTGCT 2665
 Db 2277 TCTTTTCTGTGAACCAAAAGCAAGTATGCTGATCTCTCTCTTTCTGGGGCTGCT 2336
 Qy 2666 GGGGGTCAAGCTTTATGAGCACCACCGAGTGAAGACGGGCTGAGACTTACGAGCAATTGT 2725
 Db 2337 GGGGGTCAAGCTTTATGAGCACCACCGAGTGAAGACGGGCTGAGACTTACGAGCAATTGT 2396
 Qy 2726 ACCTCGGGAAACCAAGAAATATGACTTTATTTGCTGCACAAATTCAATATCTTTCTTTCTA 2785
 Db 2397 TCCCCGGGAAACCAAGAAATATGACTTTATGCTGCACAAATTCAATATCTTTCTTTCTA 2456
 Qy 2786 CAACATGATATAGTACCCCGAAAGCAGACTACCCGAAATACCGCACTTACTTTAGCA 2845
 Db 2457 CAACATGATATAGTACCCCGAAAGCAGACTACCCGAAATACCGCACTTACTTTAGCA 2516
 Qy 2846 CCTACACAGAGATTTAGTACAGTGAAGTATGATCTGTTGGAAGAAACAAACAGCTTCC 2905
 Db 2517 CCTTCAATAGATTTAGTACAGTGAAGTATGATCTGTTGGAAGAAACAAACAGCTTCC 2576
 Qy 2906 CAAATATGCTGCTGACTTACTTACAGAGCTGCTTACAGGAGCTTTCAGAGATGATGATGACAG 2965
 Db 2577 CCAAAATGCTGCTGACTTACTTACAGAGCTGCTTACAGGAGCTTTCAGAGATGATGACAG 2636
 Qy 2966 TGACTGGGAAACCGGAAATATCATGCCCAACAAATTACAAAGATGATGAGAGTGAAT 3025
 Db 2637 TGACTGGGAAACCGGAGATCATGCCCAACAAATTATTAATATGATGATGAGAGTGAAT 2696
 Qy 3026 CCTTGGCTTACAAACTCTGTGTGCAACCGGAGCGGCGATGAAAGCCATGAGATGAGCA 3085
 Db 2697 CCTTGGCTTACAAACTCTGTGTGCAACCGGAGCGGCGATGAAAGCCATGAGATGAGCA 2756
 Qy 3086 GTTGAATTAACACGCTTGTGTGATGCAAGATGCAATCTTAATCCAGCGCTTTTCTACAT 3145
 Db 2757 GTTGAATTAACACGCTTGTGTGATGCAAGATGCAATCTTAATCCAGCGCTTTTCTACAT 2816
 Qy 3146 CTACCTGAGCGGCTTGGGTGACAGCAAGCCCGGTGCGATGCTGTGCTCCAGGCCAACAAT 3205
 Db 2817 CTACCTGAGCGGCTTGGGTGACAGCAAGCCCGGTGCGATGCTGTGCTCCAGGCCAACAAT 2876
 Qy 3206 CCGGCGACACCGACAGAAATGGGTCCAGCAAGCCGAGCTACATGCTGAAACAAAGGCT 3265
 Db 2877 CCGGCGCTTACCGGCGAGGTGGGTCCATGCAAAAGCGAGTACATGCCAGAACCAAGGCT 2936
 Qy 3266 GAGAAATCCCGGCGACAGAGCCCATGAGATGCCCAAGTTCCTTTCTACCTCAACGGGTT 3325
 Db 2937 GAGAAATCCCGGCGACAGAGCCCATGAGATGCTCAAGTTCCTTTCTACCTCAACGGGCT 2996
 Qy 3326 GGGGACACCTTACAGACTTTTGGAGGCAATTGAAAAGTTAAGACACTCTGAGCAACTA 3385
 Db 2997 AGGAGACACCTTACAGACTTTTGGAGGCAATTGAAAAGTTAAGACACTCTGAGCAACTA 3056
 Qy 3386 TACGAGCCTGGGGCTGTCCAGTTACCCCAAGGCTACCCCTTCTCTTCTGTGGAGCAGTA 3445
 Db 3057 TACGAGCCTGGGGCTGTCCAGTTACCCCAAGGCTACCCCTTCTCTTGTGGAGCAGTA 3116
 Qy 3446 CATGGGCTCCCGGCACTGGGTGCTGCTGCTTATAGGCTGGTGTGGCTGTGACATTTCT 3505
 Db 3117 CATGAGCCTGGCGCACTGGGTGCTGCTTATCAGGCTGGTGTGGCTGTGACATTTCT 3176
 Qy 3506 CGTGTGCGTGTCTTCTTGTGAACCCCTGAGCGGCGGAGATGATGATGATGCTGTGCG 3565
 Db 3177 AGTGTGCGAGTCTTCTCTGTGAACCCCTGAGCGGCGGAGATGATGATGATGCTGTGCG 3236

Qy 3566 GCTGATGACGGTTCGAGCTGTGTGGCAATGATGGGCTTCATGGAATCAAGCTAGTCCGT 3625
 Db 3237 TCTGATGACGGTTCGAGCTGTGTGGCAATGATGGGCTTCATGGAATCAAGCTAGTCCGT 3296
 Qy 3626 GCGCGTGGTTCATCTGATGCTTCTGTTGCAATGAGAGTGAAGTCAACCGTTCACGTTGC 3685
 Db 3297 GCGTGTGGTTCATCTGATGCTTGTGGCAATGAGAGTGAAGTTCACCGTTCACGTTGC 3356
 Qy 3686 TTTGGCTTTTCTGAGAGGCGCATGGGCGACAAAGAACCGAGGGCTGTGCTTCCCTGAGCA 3745
 Db 3357 TTTGGCTTTTCTGAGAGGCGCATGGGCGACAAAGAACCGAGGGCTGTGCTTCCCTGAGCA 3416
 Qy 3746 CATGTTTGCACCGCTCTGATGAGGCGCGGTGTCACATCTGCTGGAGTGGTGAATGCTGCGC 3805
 Db 3417 CATGTTTGTCTCCGTTCTGAGAGGCTGTGTGTCACATCTGCTGGAGTGGTGAATGCTGCGC 3476
 Qy 3806 GGGATCTGAGTTCGACTTCATTTGTCAAGTATTTCTTTGCTGTGCTGGCGATCTCCACCAT 3865
 Db 3477 AGGGTCCGAATTTGATTTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3536
 Qy 3866 CCTGCGGCTTCTCATGAGCTGGCTGTTTCTTCCGCTGTTTCTTCTTCTTGGACATA 3925
 Db 3537 CTGGGGGTTTCTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 3596
 Qy 3926 TCTGAGGTTGCTCCAGCCCAAGGCTTGAACCGGCTGCGCCACACCGCTTCCCTGAGCCACC 3985
 Db 3597 TCTGAGGTTGCTCCAGCCCAAGGCTTGAACCGGCTGCGCCACACCGCTTCCCTGAGCCACC 3656
 Qy 3986 CCCCAGCGTGTCCGCTTCCGATGAGCGCGCGCCGACACGACGAGCGGCTCTGATTTCTC 4045
 Db 3657 TCCAAGTGTGCTCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3716
 Qy 4046 CGACTCGGAGTATATTTCCCAACGACAGTATGAGCTTACGAGAGAGCTTGGGCACTA 4105
 Db 3717 CGACTCGGAGTATATTTCCCAACGACAGTATGAGCTTACGAGAGAGCTTGGGCACTA 3776
 Qy 4106 CGAGCGCCAGAGGAGGCGGAGGCGGCTGCGCCACCAAGTATGATGGAACCCACAGAAA 4165
 Db 3777 CGAGCGCCAGAGGAGGCGGAGGCGGCTGCGCCACCAAGTATGATGGAACCCACAGAAA 3836
 Qy 4166 CCCCCTTTCGCCCCACTCCACTGTGTGTCATCCGGAATCCAGGATCACCCACCTTCGAA 4225
 Db 3837 CCCCCTTTCGCCCCACTCCACTGTGTGTCATCCGGAATCCAGGATCACCCACCTTCGAA 3896
 Qy 4226 CCGGAGNAGAGACCCCACTGAGTCTGAGGCTTCCCTGCTCCGAGCGGAGGCAAGCA 4285
 Db 3897 CCGGAGNAGAGACCCCACTGAGTCTGAGGCTTCCCTGCTCCGAGCGGAGGCAAGCA 3956
 Qy 4286 GCCCGCAGGAGCCCGCCAGAGAGGCTTGGGCGCACCCCTGTACAGACCGGCGAGAGA 4345
 Db 3957 GCCCGCAGAGGAGTCCCTTAGAGAGAGGCTTGGGCGCACCCCTGTACAGACCGGCGAGAGA 4016
 Qy 4346 CGCTTTTGAATTTCTACTGAAGGCGATTTCTGGCCTTACCAATAGGCGCCGCTGGGCGCC 4405
 Db 4017 CGCTTTTGAATTTCTACTGAAGGCGATTTCTGGCCTTACCAATAGGCGCCGCTGGGCGCC 4076
 Qy 4406 TCGGGGGCGGCTTCTACAAACCTCGGAAACCGAGGCTCACTGCTCATGGGCAAGCTCGT 4465
 Db 4077 TCGGGGGCGGCTTCTACAAACCTCGGAAACCGAGGCTCACTGCTCATGGGCAAGCTCGT 4136
 Qy 4466 GCCCGGCTTACGAGCCCATCAACAGCTTGAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 4525
 Db 4137 GCCCGGCTTACGAGCCCATCAACAGCTTGAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 4196
 Qy 4526 GCACCCGCGGCTTCTGAGGCGTGGGCGGAACCCCGAGGCGGAGCTGTGCCAG--- 4581
 Db 4197 GCATCCCCCG-----CCTGAGACCTGGGCGCAACCCCGAGGCGGCGGCTGTCCAGGCTA 4250
 Qy 4582 -----GCTACCTGAGAGTGAACAGGCGCTGTTTGAAGACCCCGACAGTGTGCTTCCAGT 4636
 Db 4251 TGAGAGCTTACCTGAGAGTGAACAGGCGGTATTTGAGAGATCCATGATGCTTTCATGAT 4310

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4637 CCGGTGTGAGAGGAGGATTCGAAGGTGAAGTCAATGAGCTGACGAGAGCTGGAATGCCA 4696
4311 CAGGTGTGAGAGGAGGAGCTCAAGAGTGAAGTGTATAGAGCTACAGAGCTGGAATGTGA 4370
4697 GGAGAGGCGCGGGGAGAGCAGCTCCACACTGAGGAGGATTAATCTGAAGCAAGAGGCC 4756
4371 GGAGAGGCGCGGGGAGAGCAGCTCCACACTGAGGAGGATTAATCTGAAGCAAGAGGCC 4430
4757 AAGATTTGGAAACCCCGACCCCGACCTCTTCCAGAACTGCTGCAAGAACTGGTTGG 4816
4431 AAGATTTGGAAA-GCCCGCGCCCGACCTCTTCCAGAACTGCTGCAAGAACTGGTTGG 4489
4817 AGTATGTAAGAAAGATGCCCTGTGCGAGAGCAGCTCAATGTTACTGTAAACGATTTGA 4876
4490 AATATATG-----GGAAGGCACTTCACTTGTACTGTAACTGATGTGA 4530
4877 TTAATTTGTAATATTTCTTAATATTTAAGAGATGACACATGTGAATATAGGAG 4936
4531 TTAATTKGTGAATATTTCTTAATATTTAARAGGTGACACA--TGTAAATATACATGG 4588
4937 GAAGGATGTAAGTGTATGATCTGCGGCTCTCCACTCCGCGCCCGAGTGAGGAGGCC 4996
4589 AAGAGGTGTACAGT-CTAATTCCTGGGGCTCTCCACTCTGCGCGAGGTGGAGAGCC 4647
4997 ACAGTGGGCGCTCCGATTTGTGCAATGGGCTCCGCGCAACAACCAAGCTTCATTAAG 5056
4648 ACA--GGGGCGCTTCCCGCTGTGATGATGCTGTGCGCAACAACCAAGCTTAAG 4705
5057 CTGAAA-----TTTACGATATGTTGCTGCTGCTTAATATTTGATATTTACTTGT 5108
4706 TTTTAAAAAATATCCAGAGATATGCTGCTGCTTAATATTTGATATTTACTTGT 4765
5109 TTAATTTGATCAATATTTGCTTATGATATGATATTTTAAAGTTTCTGTTAA 5168
4766 ATAATTCATGCAATATTTGCTTATGATATGATATTTTAAAGTTTCTGTTAA 4824
5169 ATATTTTAAATTTGATATTCACAAACCTGTGTAGTAAATGTTACTGTTAACTTGA 5228
4825 ATATTTTAAATTTGATATTCACAAACCTGTGTAGTAAATGTTACTGTTAACTTGA 4884
5229 AACACGCTATGCTGATATTTTGTGTTATGAGCAGATATGAAAGAAC 5280
4885 AACACGCTATGCTGATATTTTGTGTTATGAGCAGATATGAAAGAAC 4931

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RESULT 11

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US-09-060-939A-1
: Sequence 1, Application US/09060939A
: GENERAL INFORMATION:
: APPLICANT: Frederic de Sauvage, David A. Carpenter
: TITLE OF INVENTION: Patched-2
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/060,939A
: FILING DATE: 15-Apr-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Svoboda, Craig G.
: REGISTRATION NUMBER: 39,044
: REFERENCE/DOCKET NUMBER: P1405
: TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 650/225-1489
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ. ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4030 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-09-060-939A-1

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Query Match 22.2%; Score 1176.4; DB 14; Length 4030;
 Best Local Similarity 61.5%; Pred. No. 2,1e-218;
 Matches 2058; Conservative 0; Mismatches 1221; Indels 69; Gaps 8;

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QY 591 GCTACTGCGCGGAAAGCCCACTGTGCTGAGACGGAAGTTGACAGACTCTTATTTAA 650
DB 311 GCTGGAGCGCTGAAGGCTCCAGCTGCTGCTGCTTCACTTCAAGGCGCTCTCTCTCT 370
QY 651 CTGGGTTGTTACATTCAAAAAACTCGCGCAAGTTCTTGTGTGGGCGCTCTCATATTT 710
DB 371 CTGGGATGCGGGATCCAGAGCATTTGCGCAATGCTCTTCTGAGACTGTGGCTTT 430
QY 711 GGGGCGCTTGGCGGTGGGATTAAGACGCAACCTCGAGACCAACGTGAGAGCTGTGG 770
DB 431 GGGGCGCTTGGCGGTGGGATTAAGACGCAACCTCGAGACCAACCTGAGACAGCTGTGG 490
QY 771 GTGGAATTTGAGAGAGAGTAAAGTGTGAATTAATTAATCTGCGCAGAAATTTGAGAA 830
DB 491 GTAGAAATGGGACCGCGGGTGGAGAGCTGCAATTAACCAAGAAACCTGGGGAG 550
QY 831 GAGGCTATGTTAACTCAACCTCATATACAGACCCCTAAAGAAAGTGTCAATGTC 890
DB 551 GAGGCTCATATACCTCTCTGAGATGCTGATACAGACCGCAGAGAGGAGAAATTC 610
QY 891 CTGACACAGAGAGCGCTCTCAACAACCTGCACTGCGACTCCAGGCCAGCGTGCAT 950
DB 611 CTACACCCGAAAGCACTTGGCTCCACCTCCAGGACGCTTCACTGCAAGTAAATCTCAA 670
QY 951 GTATACATGTAAACAGAGCAGTGAATTTGGAATTTGTTAACTCAAGAGAGCTT 1010
DB 671 GTATACATGTAAAGAGAGCTCTGGAGATTTGAACAATCTCTACAGTCAAGAGCTTCC 730
QY 731 CTATATGAAATGGAATGATGAGTGAATGAGATGAGATGAGATGAGATGAGATGAGAT 790
QY 1011 ATCACAGAAACAGGTTACATGATGATAGATTAATTAATCTTACCTGTTGATATTT 1070
DB 791 ACACCTTTGGAGCTCTTCTGGGAAGGGGCAATTTACAGTCTGGACACCATATCTCTGA 1130
QY 1131 GGTAAACCTCTCTTGGGAGCAAACTTCCACCTTTGGAATTTCTGGAAGATTTAAAG 1190
DB 851 GCGCGCGCGGATATTCAGATGAGACCACTGATTCAGAGCAGTCTGAGAGAGCTGGGT 910
QY 1191 AAAATTAACATATCAAGTGGAGCAGCTGGGAGGAAATCTGAATTAAGCTGAGTGGTCA 1250
DB 911 CCTTTCTCTCTCTTGAAGGCTTCCGGGAG--CTGCTAGACAAAGCAGACAGTGGGCG 967
QY 1251 GGTACATGAGAGCGCGCGCTGCTCAATCCGCGCGGATCCAGACTGCGCGCGCACAGCC 1310
DB 968 GCGTACGTGGGCGCGCGCTGCTGCAACCTTATGACCTCCACACTGCACTGATGTCGCC 1027
QY 1311 AACAAAAATTCACAAACCTCTTGAATTTGAGCTTTGTTGAATGATGATGATGATGATG 1370
DB 1028 AACCATACAGCAGAGGAGCTCCCAATGTGCTGACGAGCTGAGTGGGCGCTGCATGGC 1087
QY 1371 TTAATCAGAAAGTATATGCTGAGTGGAGGAGGATTTGAGTGGTGGCAGATCAAGAAC 1430
DB 1088 TTTCCCAAAATTCATGACACTGAGAGGAAATGCTGCTGAGGAGGATGAGCAGAGAAC 1147
QY 1431 AGCACTGGAAAACCTGTCAGGCGCCATGCTCTGAGACACCATGTTCAATGATGCTGCC 1490

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Db 1802 ctgagagcctctcccaagcgagcagatggtgtgctgacattgtgacggtgagc 1861
 QY 2151 ctgattttttctgcatttctgagcattgatttatttcagacgagagacgagactggat 2210
 Db 1862 ctgtctctcccaagcactcccaagcctgagcctgagcgagcgacactgagcgctgac 1921
 QY 2211 attttctgctgtttttacagcccttgcctgacagagattgatttgcagtttgcagcc 2270
 Db 1922 gtgtctgctgtctctccagctcctgtctgtcagtgatcagatcctgtcccaag-- 1979
 QY 2271 ttagccgacacacagacatttaccgctacagcccccacaccttccctacgacacag 2330
 Db 1980 --agctggtggagcgagacagctacagtggtgcatgtgcccacactgacacagttcaagc 2037
 QY 2331 ttggccattgaaagcagatttaccagctgacgctgacgctgacgctgacgctgacgac 2390
 Db 2038 ctttacc-----cactgtgaagcagcagcagcagcagcagcagcagcagcagcagc 2084
 QY 2391 cccacacacagcagctgatttaccacacacgctgacgctgacgctgacgctgacgctgac 2450
 Db 2085 ctcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2144
 QY 2451 gttacgctgacacagacacacacacacacacacacacacacacacacacacacacacac 2510
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 Db 2288 aaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2347
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 QY 2868 gtgaagtattgtattgttgaagaaacaaacagcgttcccaaaattgctgacacttcttct 2927
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 QY 2928 aagagctgctgtttagagcactttagagatgacattttagacagtgacagtgagaaaccc 2987
 Db 2588 cgcacactgtctacaggaatccacagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2647
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 Db 2708 cagactgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2767
 QY 3108 gattgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3167
 Db 2768 gacagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2827
 QY 3168 aacgaccccggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 3227

Db 2828 agtgaacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2887
 QY 3328 gtccacgacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3387
 Db 2888 ctgcagacaaatagacacacacagcagcagcagcagcagcagcagcagcagcagcagcagc 2944
 QY 3388 atgcagttatgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3447
 Db 2945 ttgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3004
 QY 3348 gagcgaattgaaaagtaagacacatttgcacagcagcagcagcagcagcagcagcagcagc 3407
 Db 3005 gagccacatgaggggggggggggggggggggggggggggggggggggggggggggggggg 3064
 QY 3408 taccacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3467
 Db 3065 taccacaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3124
 QY 3468 ctgctgtttcattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3527
 Db 3125 ctgtgcgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3184
 QY 3528 aacccttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3587
 Db 3185 aacccttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3244
 QY 3588 ggcattgatggggcctgattggaattcagacagcagcagcagcagcagcagcagcagcagc 3647
 Db 3245 gttatcaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3304
 QY 3648 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3707
 Db 3305 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3364
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 Db 3365 ggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3424
 QY 3768 gggcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3827
 Db 3425 gggcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3884
 QY 3828 gttcaggtatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 3887
 Db 3485 gtaagtaacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 3544
 QY 3888 gttttgtcttcccggtcttcttcttcttcttcttcttcttcttcttcttcttcttct 3935
 Db 3545 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3592

RESULT 13
 US-09-207-857-1
 : Sequence 1, Application US/09207857
 : GENERAL INFORMATION:
 : APPLICANT: Buncroft, David A.
 : TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
 : FILE REFERENCE: ONV-05001
 : CURRENT APPLICATION NUMBER: US/09/207,857
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: Patent Ver. 2.0
 : SEQ ID NO 1
 : LENGTH: 4391
 : TYPE: DNA
 : ORGANISM: human
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (297)...(3905)
 US-09-207-857-1

Query Match 22.2%; Score 1173.2; DB 16; Length 4391;
 Best Local Similarity 61.4%; Pred. No. 9,1e-218;
 Matches 2056; Conservative 0; Mismatches 1223; Indels 69; Gaps 8;

QY 591 GCTACTGCGCGAAGAGCGCCCTGTGGCTGAGAGGAGATTTCAGAGACTTTATTTAA 650
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 375 gcltggagcccttgaaagccctcctcgtcgtctcctcctcctcctcctcctcctc 434
 QY 651 CTGGGCTTTAAATTCATAAAAGAGCGCAAGTCTTGGTTGGTGGCCCTCTCATATTT 710
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 435 ctggagatcgggatcccaagacatctgttgcgaagtgcctctctctctgttgcctt 494
 QY 711 GGGGCTTCGGGCTGGGATTAAGACGAGCACTCGAGACCAAGCTGAGAGAGCTGTG 770
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 495 ggggccccgttagttagtctcgcagctcgtatattgagacaacttggaaacactg 554
 QY 771 GTGAGAGTTGGAGAGAGAGTAAAGTCGTGAATTAATTATCTGCGCAGAGATTTGAGAA 830
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 555 gtagaagltggcaagccgggttagccagagctgacatcaccaagagagaagctgg 614
 QY 831 GAGGCTATGTTTAACTCACTCACTACAGAGACCCCTAAAGAGAGAGTCTATATTC 890
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 615 gaggctcgcataccctcccaatgtctgatacaagaccgacaggaagagagaacatc 674
 QY 891 CTGACACAGAGAGCGCTCTCAACACCTGAGACTCGGCACTCCAGGCCAGCTGTCAAT 950
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 675 ctcaaccccgagcaacttgcctcccaactccagcagccctcaactgcagtaagtc 734
 QY 951 GTATACATGTTACACAGGCACTGCAATTTGTGTTACAAATTCAGAGAGAGCTT 1010
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 735 gtaacactcctatgggaagctccctggagatttgaacaaactctgatacaagctg 794
 QY 1011 ATCAGAGAAAGGTTACATGATGATAGATATATCTTACCCCTTGGTTATATTT 1070
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 795 ctctctgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 854
 QY 1071 ACACCTTTGAGACTGCTTGGGAAAGGCGGAAATTAATTAATTAATTAATTAATTA 1130
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 855 accccctcgcagctctctctggaggaggagcaactccaaaggggccctccctcc 914
 QY 1131 GGTAAACCTCTTGGGCTGGGCAAACTTTCGACCTTTGGAAATTCCTGGAAGAGTTAAAG 1190
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 915 ggcgcgcgcgaatcccaatgagcccaactgagccagctgagagagagctgg 974
 QY 1191 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1250
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 975 ccccttgcctcctcttggagggttccggag---ctgctagaagaaggcaaggctgg 1031
 QY 1251 GGTATCATGACCGCCCTGCTCAATCCGCGCATCCAGACTGCCCGCCAGACGCCCC 1310
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1032 gcccagtgaggggccctgtctgacccctga tgaactccactgagtagtgccgc 1091
 QY 1311 AACAAAAATTAACCAAAACCTCTTGAATGAGCCCTTGTTCGAATGAGTCAATGAGC 1370
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 Db 1092 aacatcccaagcaagcaagctcccaatgagctcagagctgagtgaggagccatg 1151
 QY 1371 TTATTCAGAAAGTATATACACTGAGAGAGAGAGTGTGTTGGTGCGACAGTCAAGAC 1430
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 Db 1152 tttccccaacaatcactgactgagagagagatgtctgtgtggaggacatgagcagag 1211
 QY 1431 AGCACTGGAAAACTGTCAGCGCCCATGCCCTGACAGCCATTCAGTTAAATGATGCC 1490
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1212 ccccaagagagctgtctgaggagagagagagagagagagagagagagagagagag 1271
 QY 1491 AAGCAAAATGTTACGAGCACTTCAAGGGGTACGAGTATGTCACACATCACTGGAACGAG 1550
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1272 cgcagagctgtacgagcatttccgggggtgactacagacacatgacatltggag 1331
 QY 1551 GACAAAGGCGAGCCATCTGAGAGCGTGGAGAGACATATGAGAGTGGTGTATCAG 1610
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 Db 1332 gaggagagcagagagagagagagagagagagagagagagagagagagagagag 1391
 QY 1611 AGTGTGACAGAACTCCACTCAAAAGGTGCTTTCACCAACAGACAGACCTGAGAGAC 1670

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 Db 1392 gcccctgccttgaagagagcttcccccagagatccatctcctcctccacacccctgag 1451
 QY 1671 ATCTGAAATTCCTTCTGAGAGAGAGAGTCAATCCGCGCTGGCGACAGGCTACTTACTATG 1730
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1452 atctctgaatgccttctcttgaagctgagctgagctgagctgagctgagctgagct 1511
 QY 1731 CTGCGCTATGCTGTATCAACATGCTGCTGGAGAGAGTCAAGTCCAGAGAGAGAG 1790
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1512 ctgagctatgagctgtgtgacacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1571
 QY 1791 GGGCTGGCTGGCTCTGCTGTTGACAGTGTCACTGCTGAGAGAGAGAGAGAGAGAG 1850
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1572 ggccttgcgggggtgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1631
 QY 1851 TTGATGGAGATTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1910
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1632 ctgctggagcctccactcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1691
 QY 1911 GTTGTGTGATGATGATTTTCTTCTGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1970
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1692 atcgaggtgagatgagatgagatgagatgagatgagatgagatgagatgagat 1745
 QY 1971 AGAATCCCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2030
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1746 ggcacccctcccaagagagagagagagagagagagagagagagagagagagag 1805
 QY 2031 CTACAGTCATCAAGCAATGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2090
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1806 ctacacacacacacacacacacacacacacacacacacacacacacacacacac 1865
 QY 2091 CTGCGGCGCTTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2150
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1866 ctgagagctctccctcccaagagagagagagagagagagagagagagagagag 1925
 QY 2151 CTGATTTTCTGCAATTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2210
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 Db 1926 ctgtctcccaagagagagagagagagagagagagagagagagagagagagag 1985
 QY 2211 ATTTTCTGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2270
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 1986 gttctctgctgtctctcccaagagagagagagagagagagagagagagagagag 2043
 QY 2271 TACACGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2330
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 2044 -agctggggagagagagagagagagagagagagagagagagagagagagagag 2101
 QY 2331 TTGCGCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2390
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 Db 2102 ctctacc-----cactgtgagagagagagagagagagagagagagagagag 2148
 QY 2391 CCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2450
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 2149 ctcccagagagagagagagagagagagagagagagagagagagagagagagagag 2208
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 Db 2209 ctggaggggtcccaagagagagagagagagagagagagagagagagagagagag 2262
 QY 2511 GACCTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2570
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 Db 2263 cagc-----ctgcaagctccctgagagagagagagagagagagagagagagag 2291
 QY 2571 TGGACATCTCATCTTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2630
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 2292 tggaaatcttgccatcttcgagagagagagagagagagagagagagagagagagag 2351
 QY 2631 AAGTAGTGTGATCTTCTCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2690
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 Db 2352 aagagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2411
 QY 2691 CGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2750
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Db 2412 ttggtgcaagaagcgctgctgacgagatgltgctccgagggacacaaagagcatgccc 2471

QY 2751 TTTATGTCGACAAATTAATCTTTCTTCTACAACTGATATAGTACCCAGAA 2810

Db 2472 ttcttgaagccagctcaagttctctctctgaagagtgccctggagccagaggt 2531

QY 2811 GCA---GACTACCCGATATCCAGCACTTACTTTACGACCTTACAGAGATTTCACTAAC 2867

Db 2532 ggccttgaactagccacccacccacccctcttgaatctgacacagcgcttcaagttcc 2591

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Db 2892 agtgaacccctggtctgacagctccacagccacacttcaaccccccactcttgaatg 2951

QY 3228 GTCCACCAACAAAGCGATTAATCTTCTTACCTTACCTGAGCTGCTGCTGCTGCTGCTG 3287

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QY 3288 ATGAGATGATGCTGCTGCTTCTTCTTACCTTACCTGAGGCTGCGGAGACCTCACTTGTG 3347

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QY 3468 CTGCTGTCATCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3527

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QY 3528 AACCCCTGAGCGCGGAGATCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3587

Db 3249 aacccttgaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctc 3308

QY 3588 GGCATGATGGGCTCATCGGAATCAAGCTCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3647

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QY 3708 GCGCAACAAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3767

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QY 3768 GCGCGCTGTCACCTGCTGAGAGTCTGATGCTGCGGAGATGCTGCTGCTGCTGCTGCTG 3827

Db 3489 ggggcacatcctacatgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3548

QY 3828 GTACGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3887

Db 3549 gtaagtaactcttctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3608

QY 3888 GTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3935

Db 3609 gtgcgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3656

RESULT 14

US-09-060-939A-9

Sequence 9, Application US/09060939A

GENERAL INFORMATION:

APPLICANT: Frederic de Sauvage, David A. Carpenter

TITLE OF INVENTION: Patched-2

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/060,939A

FILING DATE: 15-Apr-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P1405

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ. ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2082 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double

TOPOLOGY: Linear

US-09-060-939A-9

Query Match

Best Local Similarity 11.2%; Score 593.8; DB 14; Length 2082;

Best Local Similarity 62.7%; Pred. No. 3.8e-105;

Matches 960; Conservative 0; Mismatches 562; Indels 9; Gaps 2;

QY 591 GCTACTGCGCGGAAACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650

Db 86 GCTGGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 145

QY 651 CTGGGTTGTTAATTCATAAATAAATCTGCGCAAGTCTTGTGTTGGGCTCCCTCATATT 710

Db 146 CTGGGATGCGGGATCCAGAGACATTTGCGCAAGTCTTGTGTTGGGCTCCCTCATATT 710

QY 711 GGGGCTTTCGCGGTGGGATTTAAAGCAGCAACCTCGAGCAACAGCTGAGAGCTGCTG 770

Db 206 GGGGCTTTCGCGGTGGGATTTAAAGCAGCAACCTCGAGCAACAGCTGAGAGCTGCTG 770

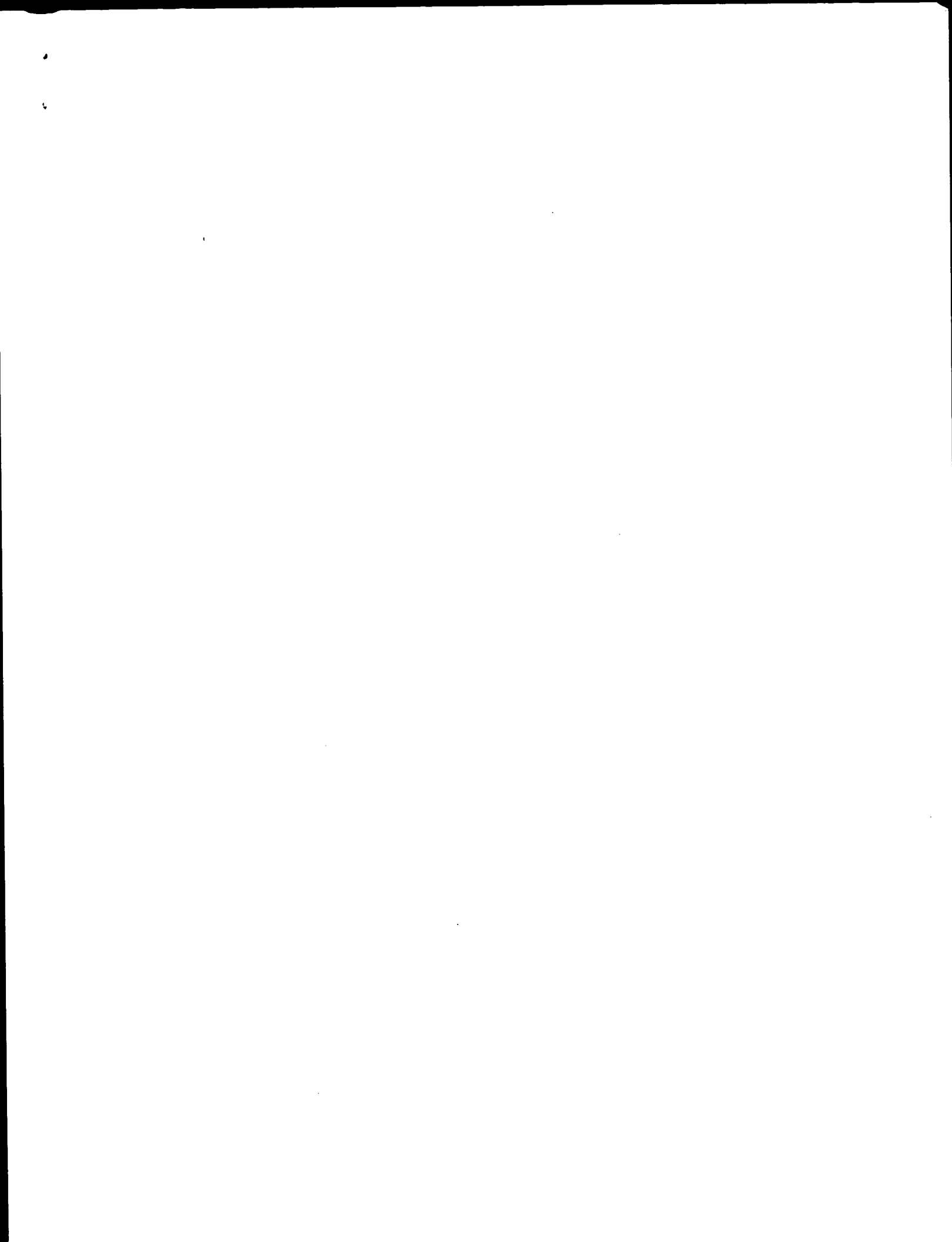
QY 771 GTGGAAGTTGGAGAGAGTAAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTA 830

Db 266 GTAGAAGTGGGAGCGCGGTGAGCGAGCTGATTAATTAATTAATTAATTAATTAATTA 830

QY 831 GAGGCTATGTTAATTCATCACTCATGATGATGATGATGATGATGATGATGATGATGATG 890

Db 326 GAGGCTGATACACCTTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 890

Db 626 ggcgcgcgagatccatgagaccacccgagcagcgtgagagcctggt 685
 QY 1191 AAAATTAACATATCAAGTACAGTGGAGAGAAATGTAATAGGCTGAGTGGTCAT 1250
 Db 686 ccccttgccctccttgagggcttcgggag--ctgctagacaagcacaagctggccag 742
 QY 1251 GGTACATGAGCCGCCCTGCTCAATCCGGCCGATCCAGACTGCCCGCCAGCCCCC 1310
 Db 743 gctacgtggcgccctgctgacccctgatgacctccactagccactagtcctccc 802
 QY 1311 AACAAAAATTCACCAAACTCTTGATATGAGCCCTTGTGATGGATGATCATGAGC 1370
 Db 803 aaccatacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 862
 QY 1371 TTATCCAGAAAGTATATGCACTGCGAGAGAGATTGATGAGTGGACAGTCAAGAAC 1430
 Db 863 ttctccacaatcatalcagcagcagcagcagcagcagcagcagcagcagcagcagc 922
 QY 1431 AGCACTGGAACACTGTCAGGCGCCATGCCCTGCAAGACATGTTCCAGTTAATGACTCCC 1490
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 QY 1491 AAGCAAAATGATGAGCACTTCAGAGGGATGAGTATGTCACATCATCACTGSAACGAG 1550
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 Db 1103 gccctgcctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1162
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 Db 1163 atcctgcatgctctctgagcagcagcagcagcagcagcagcagcagcagcagcagc 1222
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 QY 1791 GGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1850
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 Db 1343 ctgctcgacatcacttcaatgctgacacacacagcagcagcagcagcagcagcagc 1402
 QY 1911 GTTGGTGGATGATGTTTCTTCTGCGCCAGCGCTTCACTGTAACAGACAGAAATAA 1970
 Db 1403 atcgagcgtgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1456
 QY 1971 AGAATCCCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2030
 Db 1457 ggcacccctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1516
 QY 2031 CTACGCTCATAGCAATGTCACAGCCTTCTTCAATGAGCGCGTTAATCCCAATTCGCG 2090
 Db 1517 ctacatcatalcaacaacatgagcagcagcagcagcagcagcagcagcagcagcagcag 1576
 QY 2091 CTGCGGCGCTTCTCCCTCAGGAGCGGCTAG 2121
 Db 1577 ctgagagcctctccttcaagcagcagcagcagcagcagcagcagcagcagcagcag 1607



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:12:42 ; Search time 2793.3 Seconds

(without alignments)
13265.884 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288

Sequence: 1 GAATTCGGGAGCGCAAG.....TATGAGAGAGCCCGAATT 5288

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
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8: gb_est8:*
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117: em_estp16:*
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 189: em_estp78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
117: em_estp16:*	1	566	10.7	566	28	AL044174
118: em_estp17:*	2	498.4	9.4	653	106	BE263745
119: em_estp18:*	3	484.6	9.2	496	28	AL046751
120: em_estp14:*	4	462.4	8.7	475	105	BE244165
121: em_estp15:*	5	422.4	8.0	437	28	AL120137
122: em_estp16:*	6	410.4	7.8	657	104	BE109565
123: em_estp17:*	7	379	7.2	476	104	BE106695
124: em_estp18:*	8	317.6	6.0	402	19	AI326577
125: em_estp19:*	9	316	6.0	329	21	AI494319
126: em_estp15:*	10	306	5.8	422	3	AI171645
127: em_estp16:*	11	300.6	5.7	475	15	AI045038
128: em_estp17:*	12	300.2	5.7	305	105	BE243347
129: em_estp18:*	13	299.4	5.7	312	135	BE765294
130: em_estp19:*	14	290.4	5.7	314	17	AI239549
131: em_estp20:*	15	290.4	5.5	511	91	AW528449
132: em_estp21:*	16	289.8	5.5	585	159	AO608259
133: em_estp22:*	17	288.8	5.5	336	3	AA169807
134: em_estp23:*	18	287.2	5.4	403	2	AA080038
135: em_estp24:*	19	275	5.2	464	1	AA030749
136: em_estp25:*	20	269.8	5.0	473	107	BE335795
137: em_estp26:*	21	263.4	4.9	310	5	AA328411
138: em_estp27:*	22	259.4	4.8	273	26	AI880090
139: em_estp28:*	23	253.4	4.7	580	173	AZ498012
140: em_estp29:*	24	249.2	4.7	397	89	AW314277
141: em_estp30:*	25	243.6	4.6	436	106	BE292080
142: em_estp31:*	26	243	4.5	550	135	BE757000
143: em_estp32:*	27	240	4.5	253	21	AI494442
144: em_estp33:*	28	239	4.5	451	8	AA517095
145: em_estp34:*	29	214.8	4.1	495	137	BE938361
146: em_estp35:*	30	193.2	3.7	316	102	BE188695
147: em_estp36:*	31	186.4	3.5	331	5	AA329006
148: em_estp37:*	32	177.6	3.4	184	15	AI018356
149: em_estp38:*	33	176	3.3	1101	190	CNS017V5
150: em_estp39:*	34	156.4	3.0	364	23	AI705049
151: em_estp40:*	35	156	3.0	946	192	CNS03EU0
152: em_estp41:*	36	153.6	2.9	285	102	BE190274
153: em_estp42:*	37	140	2.6	287	136	BE843857
154: em_estp43:*	38	137	2.6	201	25	AI842476
155: em_estp44:*	39	136.2	2.6	1022	192	CNS03EU0
156: em_estp45:*	40	124.4	2.4	175	26	AI885389
157: em_estp46:*	41	122.8	2.3	513	165	AZ012766
158: em_estp47:*	42	118.2	2.2	689	106	BE282024
159: em_estp48:*	43	116.6	2.2	375	139	C63129
160: em_estp49:*	44	116	2.2	573	105	BE234509
161: em_estp50:*	45	102.2	1.9	279	149	AO097628

ALIGNMENTS

RESULT 1
 LOCUS AL044174 566 bp mRNA
 DEFINITION DKFZP434P0428.L1 434 (synonym: htes3) Homo sapiens CDNA clone
 ACCESSION AL044174
 VERSION AL044174.1 GI:5432399
 KEYWORDS EST.
 SOURCE human.

29-FEB-2000

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Bioecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Bloecker H
MIPS
Am Klopfersplitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Braunschweig/Germany) within the CDNA sequencing consortium of the
German Genome Project.
s1 sequence also available.
This clone (DKFZp434P0428) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Source
1..566
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434P0428"
/clone_lib="434 (synonym: htes3)"
/rissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPori1; Site_1: NotI; Site_2: SalI"

BASE COUNT 164 a 131 c 137 g 134 t

ORIGIN

Query Match 10.7%; Score 566; DB 28; Length 566;
Best Local Similarity 100.0%; Pred. No. 7.7e-129; Mismatches 0; Indels 0; Gaps 0;
Matches 566; Conservative 0;

857 GATCAGACCCCTTAAGAAAGAGTGTATGTCTCTGACACAGAAAGCGCTCTACACAGA 916
|||||
1 GATCAGACCCCTTAAGAAAGAGTGTATGTCTCTGACACAGAAAGCGCTCTACACAGA 60
917 CCTGAGCTCGGACATCCAGGCGAGCGGTGCATATACATGATCAACAGGACAGTGGAA 976
|||||
61 CCTGAGCTCGGACATCCAGGCGAGCGGTGCATATACATGATCAACAGGACAGTGGAA 120
977 ATTGGAACATTTGTGTACAATCAGAGAGCTTATCAGAAACAGTGTACATGATCA 1036
|||||
121 ATTGGAACATTTGTGTACAATCAGAGAGCTTATCAGAAACAGTGTACATGATCA 180
1037 GATAATAGATATCTTACCCCTTGTGATATATACACCTTTGGAGCTGCTTGGGAAG 1096
|||||
181 GATAATAGATATCTTACCCCTTGTGATATATACACCTTTGGAGCTGCTTGGGAAG 240
1097 GCGGAATTCACAGTCTGGGACAGCATACCTCTAGTAAACCTCTTGGCGTGGACAAA 1156
241 GCGGAATTCACAGTCTGGGACAGCATACCTCTAGTAAACCTCTTGGCGTGGACAAA 300
1157 CTTGACACCTTTGGAATCTCTCGAAGAGTTAAGAAAAATTAACATCAAGTGCAGAGCTG 1216
|||||
301 CTTGACACCTTTGGAATCTCTCGAAGAGTTAAGAAAAATTAACATCAAGTGCAGAGCTG 360
1217 GGAGAAATTCGAATTAAGAGCTGAGTTGGCATGTTACATGAGACCGCCCTGCTTAA 1276
|||||
361 GGAGAAATTCGAATTAAGAGCTGAGTTGGCATGTTACATGAGACCGCCCTGCTTAA 420
1277 TCCGGCCGATCCAGACTGCCCGCCACAGCCCAACAAAAATTCACCAAACTCTTTGA 1336
|||||
421 TCCGGCCGATCCAGACTGCCCGCCACAGCCCAACAAAAATTCACCAAACTCTTTGA 480
1337 TATGGCCCTTTGTTGAATGATGATGCTTATCCAGAAAGTATATGACTGCA 1396
|||||

Db 481 TATGGCCCTTTGTTGAATGATGATGCTTATCCAGAAATTAATATGATGCA 540
QY 1397 GGAGAGATTGATTTGGTGGACAG 1422
|||||
Db 541 GGAGAGATTGATTTGGTGGACAG 566

RESULT 2
BE263745
LOCUS BE263745 653 bp mRNA EST 13-JUL-2000
DEFINITION 601192194P1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536038 5',
RNA sequence.
ACCESSION BE263745
VERSION BE263745.1 GI:9137291
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Plate: LHCN217 row: 1 column: 23
High quality sequence stop: 645.
Location/Qualifiers
1..653
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3536038"
/clone_lib="NIH_MGC_7"
/rissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGACGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 161 a 176 c 169 g 146 t 1 others

ORIGIN

Query Match 9.4%; Score 498.4; DB 106; Length 653;
Best Local Similarity 99.8%; Pred. No. 4e-112; Mismatches 1; Indels 0; Gaps 0;
Matches 499; Conservative 0;

1233 AAGGCTGAGTTGCTATGTTACATGACCGCCCTGCTCAATCCGGCGCATCAGAC 1292
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1 AAGGCTGAGTTGCTATGTTACATGACCGCCCTGCTCAATCCGGCGCATCAGAC 60
1293 TGGCCCGCCACAGCCCGCCCAAAATTCACCAAACTCTGATATAGCCCTGTTTGG 1352
|||||
61 TGGCCCGCCACAGCCCGCCCAAAATTCACCAAACTCTGATATAGCCCTGTTTGG 120
1353 AATGCTGATGTCATGCTTATCCAGAAAGTATATGACAGGAGAGAGTTGATTTGG 1412
|||||
121 AATGCTGATGTCATGCTTATCCAGAAAGTATATGACAGGAGAGAGTTGATTTGG 180
1413 GGTGGCAGCTGCAAGAACAGCACTGGAATACTGTCAGCGCCCATGCGCTGACAGCATG 1472
|||||
181 GGTGGCAGCTGCAAGAACAGCACTGGAATACTGTCAGCGCCCATGCGCTGACAGCATG 240
1473 TTCCAGTTAATGACTCCCAAGCAAAATGTACAGACACTTCAAGGGGATACAGATGTCTCA 1532
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241 TTCCAGTTAATGACTCCCAAGCAAAATGTACAGACACTTCAAGGGGATACAGATGTCTCA 300

QY 1533 CACATCACTGGAACGAGACAAACGGCAGCCATCTGTGAGGCTTGGAGAGACATAT 1592
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 Db 301 CACATCACTGGAACGAGACAAACGGCAGCCATCTGTGAGGCTTGGAGAGACATAT 360
 QY 1593 GTGAGAGTGTTCATCAGAGTGTGCGACAGAACTCCATCAAAAGGTGCTTCCCTCACC 1652
 |||||||
 Db 361 GTGAGAGTGTTCATCAGAGTGTGCGACAGAACTCCATCAAAAGGTGCTTCCCTCACC 420
 QY 1653 ACCAGACCCCTGAGACATCTGTAATCTCTGTGAGTCAAGTCCGCTGGCC 1712
 |||||||
 Db 421 ACCAGACCCCTGAGACATCTGTAATCTCTGTGAGTCAAGTCCGCTGGCC 480
 QY 1713 AGCGGCTACTTACTGATGCT 1732
 |||||||
 Db 481 AGCGGCTACTTACTGATGCT 500
 RESULT 3
 AL046751 496 bp mRNA EST 29-FEB-2000
 LOCUS DKE2P4J41179_r1.434 (synonym: htes3) Homo sapiens cDNA clone
 DEFINITION DKE2P4J41179 5', mRNA sequence.
 ACCESSION AL046751
 VERSION AL046751.1 GI:5434813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 496)
 AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 TITLE EST (Poustka, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Poustka A.J.
 Department Lemnach
 Max-Planck-Institute for Molecular Genetics
 Ihnestrasse 73, 14195 Berlin, Germany
 Tel: +49-30-84131623
 Fax: +49-30-84131128
 Email: poustka@imping-berlin-dahlem.mpg.de
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the CDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.
 This clone (DKE2P4J41179) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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 Best Local Similarity 99.2%; Pred. No. 9.5e-109;
 Matches 487; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4798 CTTAAGAGAACTGTTGAGTTATGAAAGATGCCCTGTGCCAGACAGATTCATT 4857
 |||||||
 Db 1 CTTAAGAGAACTGTTGAGTTATGAAAGATGCCCTGTGCCAGACAGATTCATT 60
 QY 4858 GTTACTGTAACCGATTGTATTATTGTTAAATATTCTATAAATTATTAAGAGATGTAC 4917

|||||||
 Db 61 GTTACTGTAACCGATTGTATTATTGTTAAATATTCTATAAATATTGAAGATGTAC 120
 QY 4918 ACATGTATATATAGGAAGAGATGTAAAGTGTATGATCTGGGCTTCTCCACTCT 4977
 |||||||
 Db 121 ACATGTATATATAGGAAGAGATGTAAAGTGTATGATCTGGGCTTCTCCACTCT 180
 QY 4978 GCCCAGAGTGTGAGGCGACAGTGGGCGCTCCGCTTTTGTGATGGGCTCCGTCGC 5037
 |||||||
 Db 181 GCCCAGAGTGTGAGGCGACAGTGGGCGCTCCGCTTTTGTGATGGGCTCCGTCGC 240
 QY 5038 ACAACCAAGCTTTCATTTACTCTTAAATTTTCAGCATATGTTCTGCTTAAATTTGAT 5097
 |||||||
 Db 241 ACAACCAAGCTTTCATTTACTCTTAAATTTTCAGCATATGTTCTGCTTAAATTTGAT 300
 QY 5098 AATTACTGTATATTTCTATGCAAAATTTGTTTATGTAATGATTTATTTGTAAGGT 5157
 |||||||
 Db 301 AATTACTGTATATTTCTATGCAAAATTTGTTTATGTAATGATTTATTTGTAAGGT 360
 QY 5158 TTCTGTTAAATATATTTTAAATTTTCATATCAACACCCCTGTGTATGTAATGTAATCT 5217
 |||||||
 Db 361 TTCTGTTAAATATTTTAAATTTTCATATCAACACCCCTGTGTATGTAATGTAATCT 420
 QY 5218 GTTAACCTTTCACCAACCGCTATGCTGATATTTTGTGTTAATGACAGATATGAAGA 5277
 |||||||
 Db 421 GTTAACCTTTCACCAACCGCTATGCTGATATTTTGTGTTAATGACAGATATGAAGA 480
 QY 5278 AGCCCGAATT 5288
 |||||||
 Db 481 AGCCCGAATT 491
 RESULT 4
 BE244165 475 bp mRNA EST 13-JUL-2000
 LOCUS TCBAP1258 pediatric pre-B cell acute lymphoblastic leukemia
 DEFINITION Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP1258, mRNA
 sequence.
 ACCESSION BE244165
 VERSION BE244165.1 GI:9095905
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 475)
 AUTHORS Wei, Y., Tsang, Y.T.M., Mel, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.
 TITLE Pediatric Leukemia cDNA Sequencing Project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Dr. Judith F. Margolin
 Human Genome Sequencing Center at Baylor College of Medicine and
 Texas Children's Cancer Center
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713 770 4536
 Fax: 713 770 4038
 Email: jmargin@lelccc.org
 Seq primer: M13 primer.
 FEATURES
 source
 1. .475
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TCBAP1258"
 /clone_lib="pediatric pre-B cell acute lymphoblastic
 leukemia Baylor-HGSC project-TCBA"
 /sex="male"
 /tissue.type="leukocytes"
 /cell_type="pre-B cell"
 /dev_stage="pediatric 2 years"
 /lab_host="DH10B"
 /note="Vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI;
 first strand cDNA was primed with an anchored
 XhoI-Oligo(dT) primer [5'CGAGGACCTGCGCGCCGACGAGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGATCCGGCCGATTAATTAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda PSB vector. Library went through one round of normalization. Library was constructed by Wei Yu

BASE COUNT 95 a 151 c 141 g 86 t 2 others
ORIGIN

Query Match 8.7%; Score 462.4; DB 105; Length 475;
Best Local Similarity 98.3%; Pred. No. 2.9e-103;
Matches 466; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

4395 CGCTGGGGGCGCTCGGGGGCGCTTTCACAAACCTCGGAACCCAGCGCTCCATCGCATG 4454
|||||
Db CGCTGGGGGCGCTCGGGGGCGCTTTCACAAACCTCGGAACCCAGCGCTCCATCGCATG 61
4455 GGCAGCTCCGTGCGCGCTACTGCGACGCCATACACACTGTGACGGCTTCTCCCTG 4514
|||||
Db GGCAGCTCCGTGCGCGCTACTGCGACGCCATACACACTGTGACGGCTTCTCCCTG 121
4515 ACTGTGCGCGTGCACCGCGCGCTGCTTCCCTGGCGGACCCCGAGGGGACTG 4574
|||||
Db ACTGTGCGCGTGCACCGCGCGCTGCTTCCCTGGCGGACCCCGAGGGGACTG 181
4575 TGCCACAGCTACCTGACACTGACACGCGCTGTTTGAGGAGCCCGACGCTTTCAC 4634
|||||
Db TGCCACAGCTACCTGACACTGACACGCGCTGTTTGAGGAGCCCGACGCTTTCAC 241
4635 GTCCGGTGTAGAGAGGAGGATTGGAAGTGCATTTGAGCTGACAGACCTGGAATGC 4694
|||||
Db GTCCGGTGTAGAGAGGAGGATTGGAAGTGCATTTGAGCTGACAGACCTGGAATGC 301
4695 GAGAGAGGCGCGCGGAGAGAGCTCCAACTGAGGTCATTAATGAATGAGCAAGAG 4754
|||||
Db GAGAGAGGCGCGCGGAGAGAGCTCCAACTGAGGTCATTAATGAATGAGCAAGAG 361
4755 CCAAGATTGGAAGACCCCGACCCACCTTTCACAGAACTGCTGAAGAACTGGTT 4814
|||||
Db CCAAGATTGGAAGACCCCGACCCACCTTTCACAGAACTGCTGAAGAACTGGTT 421
4815 GGAGTATGGAAGAAAGATGCTGTGCGACAGACAGCTTCAATTTGACTGTAAC 4868
|||||
Db GGAGTATGGAAGAAAGATGCTGTGCGACAGACAGCTTCAATTTGACTGTAAC 475

RESULT 5
AL120137 437 bp mRNA EST 25-FEB-2000
LOCUS
DEFINITION DKF2P761G0747.t1.761 (synonym: hamy2) Homo sapiens cDNA clone
ACCESSION AL120137
VERSION AL120137.1 GI:5926036
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 437)
AUTHORS Poustka A., Klein M., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE EST (Poustka, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Imnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ). Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZP761G0747) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..437
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP761G0747"
/clone_1ib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: Not; Site_2: Salt"

BASE COUNT 76 a 121 c 122 g 117 t 1 others
ORIGIN

Query Match 8.0%; Score 422.4; DB 28; Length 437;
Best Local Similarity 99.3%; Pred. No. 2.1e-93;
Matches 434; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

4395 GCGAGCGCTACTTACTGATGCTGCGCTGCTGTAACCATGCTGCGTGGACTGCTG 1769
|||||
Db GCGAGCGCTACTTACTGATGCTGCGCTGCTGTAACCATGCTGCGTGGACTGCTG 60
1770 TCCAACTCCAGGGTGGCGGGGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1829
|||||
Db TCCAACTCCAGGGTGGCGGGGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
61 TCCAACTCCAGGGTGGCGGGGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
1830 GCAAGACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1889
|||||
Db GCAAGACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
121 GAGAGACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
1890 TTGCCATTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1949
|||||
Db TTGCCATTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
181 TTGCCATTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
1950 AGTGAACAGAGCAGATTAAGATCCCTTTGAGAGACAGACCGGGAGTGGCTGAG 2009
|||||
Db AGTGAACAGAGCAGATTAAGATCCCTTTGAGAGACAGACCGGGAGTGGCTGAG 300
241 AGTGAACAGAGCAGATTAAGATCCCTTTGAGAGACAGACCGGGAGTGGCTGAG 300
2010 GGCACAGAGCAGAGCGTGGCGCTGACGTCATCAGCAATGTCAAGCCTTCTCATG 2069
|||||
Db GGCACAGAGCAGAGCGTGGCGCTGACGTCATCAGCAATGTCAAGCCTTCTCATG 360
301 GGCACAGAGCAGAGCGTGGCGCTGACGTCATCAGCAATGTCAAGCCTTCTCATG 360
2070 GCGTTAATCCCAATTCGCGC-TCGTGGGGCGCTTCCCTCCAGGACGGTATGAGT 2128
|||||
Db GCGTTAATCCCAATTCGCGC-TCGTGGGGCGCTTCCCTCCAGGACGGTATGAGT 420
361 GCGTTAATCCCAATTCGCGC-TCGTGGGGCGCTTCCCTCCAGGACGGTATGAGT 420
421 GGTCAATTTTGGCCATGG 2145
|||||
Db GGTCAATTTTGGCCATGG 437

RESULT 6
BE109565 657 bp mRNA EST 13-JUN-2000
LOCUS
DEFINITION UI-R-BJ1-avp-f-04-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
ACCESSION BE109565
VERSION BE109565.1 GI:8501670
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 657)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB

Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mscares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares Lab Clone distribution: Clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 144-315,
 >C-rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source Location/Qualifiers

1..657
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-B01-asr-b-04-0-UI"
 /clone_1lb="UI-R-B01"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-B01
 library is a subtracted library derived from the following
 tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
 canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,
 AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
 For a detailed description of the library from which this
 clone was derived, please visit our web site at
 ratseq.eng.uiowa.edu. The subtraction has been previously
 described in (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG-Seq=None found"
 BASE COUNT 130 a 194 c 227 g 106 t
 ORIGIN

Query Match 7.8% Score 410.4; DB 104; Length 657;
 Best Local Similarity 79.4% Pseq. No. 2.2e-90;
 Matches 610; Conservative 0; Mismatches 46; Indels 112; Gaps 6;

QY 101 CGGCGGAGAGACCT-CGGGACCCCGGCAATGTGGCAATGGAAGGCGGAGGTCTGAC 159
 Db 1 CGGCGGAGAGACCTCGGCGGACATCGGCGCATGTGGCAATGGAAGGCGGAGGTCTGAG 60
 QY 160 TCCCGGAGGCGGCGGCGGCGGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 219
 Db 61 TCCCGGAGGCGGCGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 220 GCTGCTGTCATACCGGAGCCCGGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 279
 Db 121 ----GCTGTGTACCGGAGCGGAGTCTC-----CGGCGGCGGAGGAGGTCTCTCGGAG 171
 QY 280 CCGAGGCGGCGGCGGCGGCGGAGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 339
 Db 172 CCGAGGCGGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
 QY 340 GAAGCTTCCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 399
 Db 199 -----GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 231
 QY 400 ACAGCGGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
 Db 232 ACAGCGGCGG-----CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 252

QY 460 GCGCGCTGTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 519
 Db 233 GCGAGCGCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 309
 QY 520 ACCGGAGCTATGTGACACCGGCGGCGGAGCTACTGCGAGCGGCGGCGGCGGCGGCGG 579
 Db 310 ACCGGAGCTATGTGACACCGGCGGCGGAGCTACTGCGAGCGGCGGCGGCGGCGGCGG 369
 QY 580 CCAAGGGAGAGCTACTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 639
 Db 370 CCAAGGGAGAGCTACTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 429
 QY 640 TCTTATTTAACTGGGTTTACATTCATAAATAATCGGCAAGTTCTTGTTGTGGCC 699
 Db 430 TCTTATTTAACTGGGTTTACATTCATAAATAATCGGCAAGTTCTTGTTGTGGGTC 489
 QY 700 TCCTCATATTTGGGCGCTTCGCGGTGGGATTAACAGGAGCACTTCGAGACCAACTGG 759
 Db 490 TCCTCATATTTGGGCGCTTCGCGGTGGGATTAACAGGAGCACTTCGAGACCAACTGG 549
 QY 760 AGGAGCTGTGGGCGAAGTTGGAGAGCGAGTAAGTGTGAATTAATTAATTAATTAATTA 819
 Db 550 AGGAGCTGTGGGCGAAGTTGGAGAGCGAGTAAGTGTGAATTAATTAATTAATTAATTA 609
 QY 820 AGATTGGAGAGAGGCTATTTATCTCACTCACTCACTCACTCACTCACTCACTCACTCA 867
 Db 610 AGATTGGAGAGAGGCTATTTATCTCACTCACTCACTCACTCACTCACTCACTCACTCA 657

RESULT 7
 BE106695 476 bp mRNA EST 13-JUN-2000
 LOCUS BE106695
 DEFINITION UI-R-B01-asr-b-04-0-UI s1 UI-R-B01 Rattus norvegicus cDNA clone
 UI-R-B01-asr-b-04-0-UI 3', mRNA sequence.
 BE106695.1 GI:8498797
 EST.
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 476)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB

Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mscares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares Lab Clone distribution: Clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source Location/Qualifiers

1..476
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-B01-asr-b-04-0-UI"
 /clone_1lb="UI-R-B01"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The library
 (UI-R-B01) is a subtracted library derived from a mixture

	ACCESSION	A1494319
	VERSION	A1494319.1 GI:4395322
	KEYWORDS	EST.
	SOURCE	human.
	ORGANISM	Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	REFERENCE	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. 1 (bases 1 to 329)
	AUTHORS	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
	TITLE	(CGAP/BTCAP), Tumor Gene Index
JOURNAL		Unpublished (1998)
COMMENT	Contact:	Robert Strausberg, Ph.D.
	Tel:	(301) 496-1550
	Email:	Robert.Strausberg@nih.gov
	Tissue Procurement:	David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
	cDNA Library Preparation:	M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
	cDNA Library Arrayed by:	Greg Lennon, Ph.D.
	DNA sequencing by:	Washington University Genome Sequencing Center
	Clone distribution:	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: www-bio.lml.gov/btbp/image/Image.html
	Insert Length:	445 Std Error: 0.00
	Seq primer:	-400p from Gluco.
FEATURES	Location/Qualifiers	
source	1..329	/organism="Homo sapiens"
	/db_xref="taxon:9606"	
	/clone_image="2020092"	
	/clone_lib="NCI_CGAP_Brn25"	
	/tissue_type="anaplastic oligodendroglioma"	
	/lab_host="DH10B"	
	/note="Organ: brain; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAGACTGAAGTCGGAGCGGCCGCAATGCTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	41 a 125 c 140 g 23 t	
ORIGIN		
Query Match	6.0%; Score 316; DB 21; Length 329;	
Best Local Similarity	99.1%; Pred. No. 3.7e-67;	
Matches 329; Conservative 0; Mismatches 0; Indels 3; Gaps 14;		
QY	193 GGGCCCCCGGTGTGAGCACCACAGCGGTGTGTCTCTCAACGGAGCCCGACCCGAGCA	252
DB	1 GGGCCCGCGGTGTGAGCACACAGCGGTGTGTCTCTCAACGGAGCCCGACCCGAGCA	60
QY	253 GCCTGGCGGCACAGCGGTCTCTGCAAGCCGACCGCCACAGCGCCGACGAGCGCCGAGCA	312
DB	61 GCCTGGCGGCACAGCGGTCTCTGCAAGCCGACCGCCACAGCGCCGACGAGCGCCGAGCA	120
QY	313 GCGGCGACAGCGCGCGCGCGCGCGCGGAGAAGCTCCGTCCCGCGGCGGCGGCGGCGG	372
DB	121 GCGGCGACAGCGCGCGCGCGCGCGCGCGGAGAAGCTCCGTCCCGCGGCGGCGGCGG	177
QY	373 GCGGCGGCAACAATGGCTCTGGGCGGTGTAAAGCGCGCCGACGCCAGCAAGCGCGGCGGCGG	432
DB	178 GCGGCGGCAACAATGGCTCTGGGCGGTGTAAAGCGCGCCGACGCCAGCAAGCGCGGCGG	237
QY	433 GCAGCGGCTGTATTGCTGCCCGCGGAGCGCGCGGCTTGAGAGCGGAGCGCCAGACGAGCG	492
DB	238 GCAGCGGCTGTATTGCTGCCCGCGGAGCGCGCGGCTTGAGAGCGGAGCGCCAGACGAGCG	297
QY	493 GGGGGCTGGCGCGTGTCTGCCCGCGGACCGG 524	

Db	298	GGGGGCTGCGCCGCTGCTGCCCGCCGACCGG	329
RESULT	10		
LOCUS	AA171645	422 bp	mRNA
DEFINITION	z094c07.1 Stralalane cancer (#937219)		EST
ACCESSION	AA171645		23-DEC-1996
VERSION	AA171645.1		
KEYWORDS	GI:1750712		
SOURCE	EST		
ORGANISM	Human		
REFERENCE	Human sapiens		
AUTHORS	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 422)		
	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B., Chissee, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlffing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Werra, M.		
TITLE	Generation and analysis of 280,000 human expressed sequence tags		
JOURNAL	Genome Res. 6 (9), 807-828 (1996)		
MEDLINE	97044478		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev from Amersham High quality sequence stop: 285. Location/Qualifiers		
FEATURES			
source	1. .422 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:594540" /clone_lib="Stratagene ovarian cancer (#937219)" /sex="female" /dev_stage="adult, 64 years" /lab_host="SOLR (kanamycin resistant)" /note="Vector: Bluescript SK-; Site:1; EcorI; Site:2; XhoI; Cloned unidirectionally. Primer: Oligo dr. Papillary serous carcinoma, isolated from ascites, 64 year old caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector. -5' adaptor sequence: 5' GAATTCGGCAGCG 3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTTTT 3' "		
BASE COUNT	117 a 88 c 106 g 109 t		2 others
ORIGIN			
Query Match	5.8%;	Score 306;	DB 3; Length 422;
Best Local Similarity	98.1%;	Pred. NO. 1.2e-64;	
Matches 309;	Conservative 0;	Mismatches 6;	Indels 0; Gaps 0;
Db	4672	TTGAGCTGAGAGCGTGAATCGGAGAGAGAGGCCCGGGGAGAGCACTCAACTAGAGGT	4731
	1	TTGAGCTGAGAGCGTGAATCGGAGAGAGAGGCCCGGGGAGAGCACTCAACTAGAGGT	60
Db	4732	GATTAAATCTGAGCAAGAGAGGCCAAGATTGGAACCCCGCCACCCACCTCTTCCCA	4791
	61	GATTAAATCTGAGCAAGAGAGGCCAAGATTGGAACCCCGCCACCCACCTCTTCCCA	120
Db	4792	GAACTGCTGAGAGAGAGAGCTGAGAGTATGGAAGAAAGTGGCCGTGCGAGAGACGAG	4851
	121	GAACTGCTGAGAGAGAGAGCTGAGAGTATGGAAGAAAGTGGCCGTGCGAGAGACGAG	180
Db	4852	TTGATGTTAGAGTAAACCATGTTATATTTGTTAAATATTTCTAATAATTTTAAGAG	4911

